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57 3 68

From: Stucker, Jeffrey
Sent: Wednesday, January 02, 2002 9:23 AM
To: STIC-Biotech/ChemLib
Subject: 09/508552

Please search SEQ ID NO 2 from 09/508552.

Thanks,
Jeff Stucker
AU 1648
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308-4237

8E12

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Searcher: ASB
Phone: 308-4501
Location: Biotech Lab.
Date Picked Up: 1/2/02
Date Completed: 1/2/02
Searcher Prep/Review: 3 min
Clerical: 2 min
Online time: 2 min

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: ABSS02
WWW/Internet: _____
Other (specify): _____

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OM protein - protein search, using sw model

Run on: January 2, 2002, 09:56:30 ; Search time 23.85 Seconds

(without alignments)
121.126 Million cell updates/sec

Title: US-09-508-552-2

Perfect score: 204

Sequence: 1 KQIINMOEVGKAMAPISQIRIRIGRGRAVTTGK 39

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	204	100.0	39	16 AAR66409	PCUS 3-18 (421-44
2	204	100.0	39	20 AAY05339	HIV-1 CLUVAC pep
3	171	83.8	39	16 AAR66435	PCUS 3-18 (421-44
4	171	83.8	39	20 AAY05346	HIV-1 CLUVAC pep
5	155.5	76.2	150	15 AAR58552	MEAV vaccine. Syn
6	140.5	68.9	41	18 AAR32953	C3-V3 LAI immunoge
7	140.5	68.9	41	18 AAR32954	C3-V3 HB2R immunoge
8	140.5	68.9	41	18 AAR32955	C3-V3 NL43 immunog
9	140.5	68.9	41	18 AAR32956	C3-V3 MFA immunoge
10	130	63.7	41	14 AAR40194	Sequence of Peptid
11	130	63.7	41	20 AAY04026	HIV peptide T1-Sp1

12	130	63.7	53	14 AAR40193	Sequence of peptid
13	130	63.7	53	18 AAR16534	Peptide (F-T1-Sp10
14	130	63.7	229	10 AAR94802	PB1F HIV fusion p
15	127	62.3	24	14 AAR33837	Cluster peptide PC
16	127	62.3	24	16 AAR66431	PCUS 3-18 (421-44
17	127	62.3	24	20 AAY05353	HIV-1 CLUVAC pep
18	127	62.3	28	19 AAR54909	HIV gp120 envelope
19	127	62.3	32	19 AAR76910	Fusion immunoglob
20	127	62.3	68	15 AAR47845	HIV gp120 coat pro
21	127	62.3	178	13 AAR22564	Antibody specific
22	127	62.3	179	10 AAR92014	HIV portion of HTL
23	127	62.3	179	10 AAR93537	HIV portion of fus
24	127	62.3	181	15 AAR49610	HIV-1 gp120 conser
25	127	62.3	234	9 AAR81143	Sequence of fusion
26	127	62.3	234	10 AAR92010	HIV-III fusion pr
27	127	62.3	234	14 AAR31943	Recombinant PB1 fu
28	127	62.3	297	8 AAR71198	Sequence of HIV-I
29	127	62.3	319	8 AAR71199	Sequence of HIV-I
30	127	62.3	353	10 AAR92015	HIV portion of HTL
31	127	62.3	423	10 AAR92013	HIV portion of HTL
32	127	62.3	423	10 AAR93536	Sequence of HIV po
33	127	62.3	496	19 AAR37058	HIV-1 breakthrough
34	127	62.3	496	19 AAR37059	HIV-1 breakthrough
35	127	62.3	597	10 AAR93539	HIV portion of fus
36	127	62.3	640	10 AAR92012	HIV-III fusion pr
37	127	62.3	819	9 AAR81144	Sequence of fusion
38	127	62.3	819	10 AAR92011	HIV-III fusion pr
39	127	62.3	856	13 AAR25940	Modified HIV env g
40	127	62.3	863	14 AAR43869	HTLV-III ENV-LOR g
41	127	62.3	863	14 AAR43873	HTLV-III ENV-LOR g
42	127	62.3	880	18 AAR23353	Human Immunodefici
43	127	62.3	880	20 AAR73352	HIV envelope prote
44	127	62.3	880	21 AAR14844	HIV envelope prote
45	127	62.3	891	9 AAR81142	Sequence of fusion

ALIGNMENTS

RESULT 1	
AAR66409	standard; peptide; 39 AA.
XX	
AC	AAR66409;
XX	
DT	03-AUG-1995 (first entry)
XX	
DE	PCUS 3-18 (421-444) T helper site linked to HIV-1 IT18 peptide 18.
XX	
KW	T cell helper site; cytotoxic T cell response; neutralising antibody;
KW	human immunodeficiency virus type 1; envelope glycoprotein gp120;
XX	cluster peptide; principal neutralising determinant.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Region
FT	Location/Qualifiers
FT	1..24
FT	/label= PCUS 3-18 (421-444)
FT	/note= "T helper site"
FT	25..39
FT	/label= peptide_18
FT	/note= "corresponds to principal neutralising determinant of HIV gp160 V3 loop"
XX	
PD	24-NOV-1994.
XX	
PF	13-MAY-1994; 94MO-US05142.
XX	
PR	14-MAY-1993; 93US-0060988.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.

```

PA (USSH ) US SEC DEPT HEALTH.
XX
XX Ahlers JD, Berzofsky JA, Nara P, Pendleton CD, Shirai M;
PI WPI; 1995-006707/01.
XX
XX Polypeptide inducing helper T cell, cytotoxic T cell and
PT antibodies responses - to target antigen in hosts of different
PT MHC haplotypes, esp. for therapeutic or prophylactic vaccines
PT against HIV.
XX
XX Claim 15; Page 90; 120pp; English.
XX
XX Synthetic peptides spanning multideterminant regions from the HIV
CC envelope protein gp160 have been designed and are designated cluster
CC peptides (PCUS). These peptides each consist of a cluster of
CC overlapping determinants and are known to induce in vitro T cell
CC proliferation and cytokine production in mice and humans of multiple
CC MHC types. The cluster peptides were co-linearly synthesised at the
CC N-terminus of an immunodominant CTL determinant, Peptide 18, corresp.
CC to part of the gp160 V3 loop and principal neutralising determinant
CC region. AAR6409 is a specifically claimed example of such a peptide.
XX
XX
SQ Sequence 39 AA:

Query Match 100.0%; Score 204; DB 16; Length 39;
Best Local Similarity 100.0%; Pred. No. 5e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQIINMMQEVGKAMYPPISGQIRRIQKPGRAFTYIGK 39
Db 1 KqIImmwgevgkamypisgqirrlrpgpgrafvltgk 39

RESULT 2
AAY05339
ID AAY05339 standard; peptide; 39 AA.
XX
XX AAY05339;
AC
XX
XX 29-JUN-1999 (first entry)
DT
XX
XX HIV-1 CUUVAC peptide; SEQ ID NO. 2.
DE
XX
XX HIV-1; CUUVAC; cluster peptide vaccine construct; cytotoxic T lymphocyte;
KW protective mucosal CTL response; hepatitis A virus; papilloma virus;
KW feline immunodeficiency virus; feline leukaemia virus; M. tuberculosis;
KW Listeria monocytogenes; M. leprae; Giardia lamblia;
KW immune response induction.
XX
XX Human immunodeficiency virus type 1.
OS
XX
XX WO9912563-A2.
PN
XX
XX 18-MAR-1999.
PD
XX
XX 11-SEP-1998; 98WO-US19028.
PF
XX
XX 17-FEB-1998; 98US-0074894.
PR
XX
XX 11-SEP-1997; 97US-0058523.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICE.
PA
XX
XX Beljakov IM, Berzofsky JA, Derby MA, Kelsall BL;
PI Strober W;
XX
XX WPI; 1999-243663/20.
DR
XX
XX Method for inducing a protective mucosal cytotoxic T lymphocyte
PT immune response
PT
XX
XX Claim 21; Page 55; 86pp; English.

```

```

XX This sequence represents a HIV-1 cluster peptide vaccine conjugate
CC (CUUVAC) sequence. The invention relates to a method for inducing a
CC protective mucosal cytotoxic T lymphocyte (CTL) response in a mammalian
CC subject, which comprises contacting a mucosal tissue of the subject with
CC a composition comprising a purified soluble antigen. The method can
CC induce a protective mucosal CTL response in a subject. The method can be
CC used for protection against e.g. hepatitis A virus, papilloma virus,
CC feline immunodeficiency virus, feline leukaemia virus, Listeria
CC monocytogenes, M. tuberculosis, M. leprae, or Giardia lamblia. The method
CC induces long-lasting protective mucosal immune responses.
XX
XX
SQ Sequence 39 AA:

Query Match 100.0%; Score 204; DB 20; Length 39;
Best Local Similarity 100.0%; Pred. No. 5e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQIINMMQEVGKAMYPPISGQIRRIQKPGRAFTYIGK 39
Db 1 KqIImmwgevgkamypisgqirrlrpgpgrafvltgk 39

RESULT 3
AAR6435
ID AAR6435 standard; peptide; 39 AA.
XX
XX AAR6435;
AC
XX
XX 03-AUG-1995 (first entry)
DT
XX
XX PCUS 3-18 (421-444) T helper site linked to HIV-1 MN peptide 18.
DE
XX
XX T cell helper site; cytotoxic T cell response; neutralising antibody;
KW human immunodeficiency virus type 1; envelope glycoprotein gp120;
KW cluster peptide; principal neutralising determinant.
XX
XX
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
FH 1..24
FT Region /label= PCUS_3-18-(421-444)
FT /note= "T helper site"
FT 25..39
FT Region /label= peptide_18
FT /note= "corresponds to principal neutralising
FT determinant of HIV gp160 V3 loop"
XX
XX
XX WO9426785-A.
PN
XX
XX 24-NOV-1994.
PD
XX
XX 13-MAY-1994; 94WO-US05142.
PF
XX
XX 14-MAY-1993; 93US-0060988.
PR
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH ) US SEC DEPT HEALTH.
XX
XX Ahlers JD, Berzofsky JA, Nara P, Pendleton CD, Shirai M;
PI WPI; 1995-006707/01.
XX
XX Polypeptide inducing helper T cell, cytotoxic T cell and
PT antibodies responses - to target antigen in hosts of different
PT MHC haplotypes, esp. for therapeutic or prophylactic vaccines
PT against HIV.
XX
XX Claim 15; Page 90; 120pp; English.
XX
XX Synthetic peptides spanning multideterminant regions from the HIV
CC envelope protein gp160 have been designed and are designated cluster

```

CC peptides (PCIUS). These peptides each consist of a cluster of
 CC overlapping determinants and are known to induce in vitro T cell
 CC proliferation and cytokine production in mice and humans of multiple
 CC MHC types. The cluster peptides were co-linearly synthesized at the
 CC N-terminus of an immunodominant CTL determinant. Peptide 18, corresp.
 CC to part of the gp160 V3 loop and principal neutralising determinant
 CC region. AAR66435 is a specifically claimed example of such a peptide.
 XX
 SQ Sequence 39 AA;

Query Match 83.8%; Score 171; DB 16; Length 39;
 Best Local Similarity 91.7%; Pred. No. 5e-14;
 Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 KOIINMGEVGRKAMVAPISQIRIRIQRGPGRAVFT 36
 |||||||
 DB 1 KqIIMMGEVGRKAMVAPISQIRIRIQRGPGRAVFT 36

RESULT 4
 AAY05346
 ID AAY05346 standard; peptide; 39 AA.
 XX
 AC AAY05346;

DT 29-JUN-1999 (first entry)

DE HIV-1 CLUVAC peptide, SEQ ID NO. 9.

XX
 XX HIV-1 CLUVAC; cluster peptide vaccine construct; cytotoxic T lymphocyte;
 KW protective mucosal CTL response; hepatitis A virus; papilloma virus;
 KW feline immunodeficiency virus; feline leukemia virus; M. tuberculosis;
 KM Listeria monocytogenes; M. leprae; Giardia lamblia;
 KM immune response induction.

XX Human immunodeficiency virus type 1.

OS WO9912563-A2.

PN 18-MAR-1999.

XX 11-SEP-1998; 98WO-US19028.

PF 17-FEB-1998; 98US-0074894.

PR 11-SEP-1997; 97US-0058523.

XX (USSH) US DEPT HEALTH & HUMAN SERVICE.

PI Beljakov IM, Berzofsky JA, Derby MA, Kelsall BL;
 PI Strober W;

DR WPI, 1999-243663/20.

XX Method for inducing a protective mucosal cytotoxic T lymphocyte
 PT immune response

PS Claim 21; Page 55; 86pp; English.

XX This sequence represents a HIV-1 cluster peptide vaccine conjugate
 CC (CLUVAC) sequence. The invention relates to a method for inducing a
 CC protective mucosal cytotoxic T lymphocyte (CTL) response in a mammalian
 CC subject, which comprises contacting a mucosal tissue of the subject with
 CC a composition comprising a purified soluble antigen. The method can
 CC induce a protective mucosal CTL response in a subject. The method can be
 CC used for protection against e.g. hepatitis A virus, papilloma virus,
 CC feline immunodeficiency virus, feline leukemia virus, Listeria
 CC monocytogenes, M. tuberculosis, M. leprae, or Giardia lamblia. The method
 CC induces long-lasting protective mucosal immune responses.

XX Sequence 39 AA;

Query Match 83.8%; Score 171; DB 20; Length 39;
 Best Local Similarity 91.7%; Pred. No. 5e-14;
 Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 KOIINMGEVGRKAMVAPISQIRIRIQRGPGRAVFT 36
 |||||||
 DB 1 KqIIMMGEVGRKAMVAPISQIRIRIQRGPGRAVFT 36

RESULT 5
 AAR58552
 ID AAR58552 standard; Protein; 150 AA.
 XX
 AC AAR58552;

DT 29-MAR-1995 (first entry)

DE MEAV vaccine.

XX HIV-1; V3 loop; multiple epitope; AIDS; vaccine; MEAV;
 KW Escherichia coli; PKR-MEAV.

OS Synthetic.

XX Location/Qualifiers

FT 1..29 /label= CD4_binding_domain

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

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FT Peptide

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FT Peptide

FT Peptide

WO9418234-A.
 18-AUG-1994.
 PD 10-FEB-1994; 94WO-US01523.
 XX 10-FEB-1993; 93US-0015770.
 PR (UNBI-) UNITED BIOMEDICAL INC.
 XX Shen DF, Wang CY;
 PI WPI, 1994-279687/34.
 DR N-PSDB; AA070535.
 XX New recombinant proteins contg multiple antigenic determinants -
 PT linked by flexible hinge domains
 XX

PS Disclosure: Page 37-38; 56pp; English.

XX MEAV gene encodes a portion of the CD4 binding domain (AAR58550)

CC of HIV env protein, the domain being capable of inducing a helper T-

CC cell response, and 5 peptide domains from the V3 loop of HIV-1

CC isolates MN, SC, RF, IIB and WMJ2 (AAR58545-49), each peptide being

CC separated by a spacer domain (AAR58551). The gene was expressed in E.

CC coli BL21/pKK-MEAV for preparation of a multiple epitope AIDS

CC vaccine.

XX

SO Sequence 150 AA;

Query Match 76.2%; Score 155.5; DB 15; Length 150;

Best Local Similarity 71.1%; Pred. No. 1.3e-11;

Matches 32; Conservative 1; Mismatches 3; Indels 9; Gaps 1;

OY 1 KQIINMGEVKGKAMYAPPISGQIR-----RIORGPGRAFTV 36

DB 4 kgIImmgvkgkamyrrpIsqIrcdpdpdkrIhIpgpgrafvI 48

RESULT 6

AKM32953

ID AAM32953 standard; peptide: 41 AA.

XX

AC AAM32953;

XX

DT 23-JAN-1998 (first entry)

XX

DE C3-V3 LAI immunogen construct.

XX

KW Immunogen: antigenic determinant; HIV: envelope; glycoprotein;

KW env; gp; recognition; B lymphocyte; type specific; antibody;

KW vaccine; protection; immune response; infection; neutralisation.

XX

OS Human immunodeficiency virus.

OS Synthetic.

XX

PN WO9714436-A1.

XX

PD 24-APR-1997.

XX

PF 18-OCT-1996; 96WO-US16911.

XX

PR 09-FEB-1996; 96US-0599266.

PR 20-OCT-1995; 95US-0546515.

XX

PA (UYDU-) UNITV DUKE.

XX

PI Haynes BF, Parker TJ;

XX

DR WPI: 1997-244862/22.

XX

PT Synthetic human immunodeficiency virus vaccine - comprising

PT hydrophilic peptide corresponding to at least 1 antigenic

PT determinant of envelope glyco:protein recognised by B lymphocytes

XX

PS Example 11; Page 60j; 104pp; English.

XX

XX The present sequence, which comprises at least 1 antigenic

CC determinant of human immunodeficiency virus (HIV) envelope (env)

CC glycoprotein (gp) recognised by B lymphocytes, when covalently

CC linked to a carrier molecule, induces the production of high

CC titres of protective, type specific anti-HIV antibodies (Ab) in a

CC mammal. The peptide can be used in vaccines for producing a

CC neutralising immune response to HIV infection, while a HIV

CC neutralising Ab can be induced in a primate by administering a

CC composition comprising HIV env peptides that disrupt gp120/gp41

CC interactions.

XX

SO Sequence 41 AA;

Query Match 68.9%; Score 140.5; DB 18; Length 41;

Best Local Similarity 73.2%; Pred. No. 2.6e-10;

Matches 30; Conservative 1; Mismatches 7; Indels 3; Gaps 1;

OY 1 KQIINMGEVKGKAMYAPPISGQIR---RIORGPGRAFTV 38

DB 1 kgIImmgvkgkamyatrpnnntkIsrIlgpgrafvI 41

RESULT 7

AKM32954

ID AAM32954 standard; peptide: 41 AA.

XX

AC AAM32954;

XX

DT 23-JAN-1998 (first entry)

XX

DE C3-V3 HXB2R immunogen construct.

XX

KW Immunogen: antigenic determinant; HIV: envelope; glycoprotein;

KW env; gp; recognition; B lymphocyte; type specific; antibody;

KW vaccine; protection; immune response; infection; neutralisation.

XX

OS Human immunodeficiency virus.

OS Synthetic.

XX

PN WO9714436-A1.

XX

PD 24-APR-1997.

XX

PF 18-OCT-1996; 96WO-US16911.

XX

PR 09-FEB-1996; 96US-0599266.

PR 20-OCT-1995; 95US-0546515.

XX

PA (UYDU-) UNITV DUKE.

XX

PI Haynes BF, Parker TJ;

XX

DR WPI: 1997-244862/22.

XX

PT Synthetic human immunodeficiency virus vaccine - comprising

PT hydrophilic peptide corresponding to at least 1 antigenic

PT determinant of envelope glyco:protein recognised by B lymphocytes

XX

PS Example 11; Page 60j; 104pp; English.

XX

XX The present sequence, which comprises at least 1 antigenic

CC determinant of human immunodeficiency virus (HIV) envelope (env)

CC glycoprotein (gp) recognised by B lymphocytes, when covalently

CC linked to a carrier molecule, induces the production of high

CC titres of protective, type specific anti-HIV antibodies (Ab) in a

CC mammal. The peptide can be used in vaccines for producing a

CC protective immune response to HIV infection, while a HIV

CC neutralising Ab can be induced in a primate by administering a

CC composition comprising HIV env peptides that disrupt gp120/gp41

CC interactions.

XX

SO Sequence 41 AA;

Query Match 68.9%; Score 140.5; DB 18; Length 41;

Best Local Similarity 73.2%; Pred. No. 2.6e-10;

Matches 30; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

OY 1 KQIINMGEVKGKAMYAPPISGQIR---RIORGPGRAFTV 38

DB 1 kgIImmgvkgkamyatrpnnntkIsrIlgpgrafvI 41

RESULT 8

AKM32955

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ID AAM32955 standard; peptide: 41 AA.
XX
AC AAM32955;
XX
DT 23-JAN-1998 (first entry)
XX
DE C3-V3 NL43 immunogen construct.
XX
KM Immunogen: antigenic determinant; HIV; envelope; glycoprotein;
KM env; gp; recognition; B lymphocyte; type specific; antibody;
KM vaccine; protection; immune response; infection; neutralisation.
XX
OS Human immunodeficiency virus.
OS Synthetic.
PN WO9714436-A1.
XX
PD 24-APR-1997.
XX
PF 18-OCT-1996; 96MO-US16911.
XX
PR 09-FEB-1996; 96US-0599266.
XX
PR 20-OCT-1995; 95US-0546515.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Haynes BF, Palker TJ;
XX
DR WPI: 1997-244862/22.
XX
PT Synthetic human immunodeficiency virus vaccine - comprising
PT hydrophilic peptide corresponding to at least 1 antigenic
PT determinant of envelope glyco:protein recognised by B lymphocytes
XX
PS Example 11; Page 60j; 104pp; English.
XX
CC The present sequence, which comprises at least 1 antigenic
CC determinant of human immunodeficiency virus (HIV) envelope (env)
CC glycoprotein (gp) recognised by B lymphocytes, when covalently
CC linked to a carrier molecule, induces the production of high
CC titres of protective, type specific anti-HIV antibodies (Ab) in a
CC mammal. The peptide can be used in vaccines for producing a
CC protective immune response to HIV infection, while a HIV
CC neutralising Ab can be induced in a primate by administering a
CC composition comprising HIV env peptides that disrupt gp120/gp41
CC interactions.
CC
XX
SQ Sequence 41 AA;

Query Match 68.9%; Score 140.5; DB 18; Length 41;
Best Local Similarity 73.2%; Pred. No. 2.6e-10;
Matches 30; Conservative 1; Mismatches 7; Indels 3; Gaps 1;

OY 1 KOIINMOEYKAMYAPPISGQIR--RIORGPGRFVTTG 38
   ||||||||||||| : | |||||||||||||
Db 1 kqfinmwgevgkamyaatrpnntkksirirgprafvlig 41

RESULT 9
AAM32955
ID AAM32955 standard; peptide: 41 AA.
XX
AC AAM32955;
XX
DT 23-JAN-1998 (first entry)
XX
DE C3-V3 MFA immunogen construct.
XX
KM Immunogen: antigenic determinant; HIV; envelope; glycoprotein;
KM env; gp; recognition; B lymphocyte; type specific; antibody;
KM vaccine; protection; immune response; infection; neutralisation.
XX

```

```

OS Human immunodeficiency virus.
OS Synthetic.
PN WO9714436-A1.
XX
PD 24-APR-1997.
XX
PF 18-OCT-1996; 96MO-US16911.
XX
PR 09-FEB-1996; 96US-0599266.
XX
PR 20-OCT-1995; 95US-0546515.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Haynes BF, Palker TJ;
XX
DR WPI: 1997-244862/22.
XX
PT Synthetic human immunodeficiency virus vaccine - comprising
PT hydrophilic peptide corresponding to at least 1 antigenic
PT determinant of envelope glyco:protein recognised by B lymphocytes
XX
PS Example 11; Page 60j; 104pp; English.
XX
CC The present sequence, which comprises at least 1 antigenic
CC determinant of human immunodeficiency virus (HIV) envelope (env)
CC glycoprotein (gp) recognised by B lymphocytes, when covalently
CC linked to a carrier molecule, induces the production of high
CC titres of protective, type specific anti-HIV antibodies (Ab) in a
CC mammal. The peptide can be used in vaccines for producing a
CC protective immune response to HIV infection, while a HIV
CC neutralising Ab can be induced in a primate by administering a
CC composition comprising HIV env peptides that disrupt gp120/gp41
CC interactions.
CC
XX
SQ Sequence 41 AA;

Query Match 68.9%; Score 140.5; DB 18; Length 41;
Best Local Similarity 73.2%; Pred. No. 2.6e-10;
Matches 30; Conservative 1; Mismatches 7; Indels 3; Gaps 1;

OY 1 KOIINMOEYKAMYAPPISGQIR--RIORGPGRFVTTG 38
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Db 1 kqfinmwgevgkamyaatrpnntkksirirgprafvlig 41

RESULT 10
AAR40194
ID AAR40194 standard; peptide: 41 AA.
XX
AC AAR40194;
XX
DT 05-FEB-1994 (first entry)
XX
DE Sequence of peptide construct T1-SP10IIR(A), type Th-B,
DE derived from HIV MN and HIVIIB Env gp120.
XX
KM Hybrid protein; synthetic protein; immunogenic peptide; tolerance;
KM synthetic toleragen.
XX
OS Synthetic.
XX
PN WO9315750-A.
XX
PD 19-AUG-1993.
XX
PF 10-FEB-1993; 93MO-US01207.
XX
PR 10-FEB-1992; 92US-0833429.
XX
PA (HAYN/) HAYNES B F.
XX

```

PI Haynes BF;
 XX
 DR WPI: 1993-272554/34.
 XX
 PT Inducing immune tolerance to immunogenic peptide(s) or proteins -
 PT by administering the peptide(s) or proteins coupled to a 2-20
 PT aminoacid hydrophobic peptide
 XX
 PS Example: Table 8, page 42; 65pp; English.
 XX
 CC The peptide composition and sequence (epitope type) of the
 CC synthetic peptide construct is T1(Th) SP10(B cell) and A(B cell).
 CC T1 sequence is AAs 428-443 from HIVIIIB.
 CC SP10IIIB is AAs 303-321 from HIVIIIB.
 CC (A) sequence is AAs 320-324 from HIVM and AAs 322-327 from HIVIIIB.
 CC Th = T helper cell determinant.
 CC B cell = B cell neutralising antibody determinant.
 XX
 SQ Sequence 41 AA:
 SQ

Query Match 63.7%; Score 130; DB 14; Length 41;
 Best Local Similarity 73.2%; Pred. No. 4.9e-09;
 Matches 30; Conservative 2; Mismatches 5; Indels 4; Gaps 2;

OY 1 KQIINMGEVKGKMYA--PPISGQIR--RIQRGGRFAFYTI 37
 DB 1 KqIInMgeVgKamYactrpnntlrkslrIqrpjrafvtl 41

RESULT 11
 AA04026
 ID AA04026 standard; peptide: 41 AA.
 XX
 AC AA04026;
 XX
 DT 20-DEC-1999 (first entry)
 XX
 DE HIV peptide T1-SP10IIIB(A) for use in immunogenic complex.
 XX
 KM Macroglobulin: HIV: immunogenic complex; human immunodeficiency virus;
 KW hepatitis; antigen; vaccine.
 OS
 OS Human immunodeficiency virus.
 XX
 PN WO950303-A2.
 PD 07-OCT-1999.
 XX
 PE 01-APR-1999: 99WO-US07236.
 XX
 PR 01-APR-1998: 98US-0053301.
 PR 31-MAR-1999: 99US-0053301.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Pizzo SV, Gron H;
 XX
 DR WPI: 1999-601324/51.
 XX
 PT Immune response modulator alpha-2 macroglobulin complex useful in the
 PT treatment of HIV or hepatitis -
 XX
 PS Claim 3; Page 77; 103pp; English.
 XX
 CC A stable complex comprising at least one intact biomolecule and
 CC activated alpha-2-macroglobulin (alpha-2M) having an intact bait
 CC region is claimed; in which the biomolecule is covalently bound to
 CC an amino acid residue of a cleaved thiol ester of the alpha-2M,
 CC the amino acid residue being a glutamyl residue and/or a cysteinyl
 CC residue. Preparation of the complex comprises activation of alpha-2M
 CC with a nucleophilic compound followed by incubation with the
 CC biomolecule at elevated temperature. Covalent incorporation of the

CC intact biomolecule is thus effected without use of a protease. The
 CC obtained complex may be used as an antigen for stimulating immune
 CC response, e.g. in the form of a vaccine. Enhanced presentation of the
 CC biomolecule is provided, especially for those antigens which are poorly
 CC immunogenic. Reduction of immunodominance of particular epitopes is
 CC also provided. Preferably the biomolecule is an HIV antigen or a
 CC hepatitis virus antigen, or a peptide, fragment, hybrid or chimeric
 CC peptide thereof. The present sequence is a preferred example of an HIV
 CC peptide which may be used in the complex.
 XX
 SQ Sequence 41 AA:
 SQ

Query Match 63.7%; Score 130; DB 20; Length 41;
 Best Local Similarity 73.2%; Pred. No. 4.9e-09;
 Matches 30; Conservative 2; Mismatches 5; Indels 4; Gaps 2;

OY 1 KQIINMGEVKGKMYA--PPISGQIR--RIQRGGRFAFYTI 37
 DB 1 KqIInMgeVgKamYactrpnntlrkslrIqrpjrafvtl 41

RESULT 12
 AAR40193
 ID AAR40193 standard; peptide: 53 AA.
 XX
 AC AAR40193;
 XX
 DT 05-FEB-1994 (first entry)
 XX
 DE Sequence of peptide construct F-T1-SP10IIIB(A), type F-Th-B,
 DE derived from HIV MN and HIVIIIB Env gp120.
 XX
 KM Hybrid protein: synthetic protein; immunogenic peptide; tolerance;
 KW synthetic toleragen.
 OS
 OS Synthetic.
 XX
 PN WO9315750-A.
 PD 19-AUG-1993.
 XX
 PE 10-FEB-1993: 93WO-US01207.
 XX
 PR 10-FEB-1992: 92US-0833429.
 XX
 PA (HAYN/) HAYNES B F.
 XX
 PI Haynes BF;
 XX
 DR WPI: 1993-272554/34.
 XX
 PT Inducing immune tolerance to immunogenic peptide(s) or proteins -
 PT by administering the peptide(s) or proteins coupled to a 2-20
 PT aminoacid hydrophobic peptide
 XX
 PS Example: Table 8, page 42; 65pp; English.
 XX
 CC The peptide composition and sequence (epitope type) of the
 CC synthetic peptide construct is F-T1(Th) SP10(B cell) and A(B
 CC cell). T1 sequence is AAs 428-443 from HIVIIIB.
 CC SP00IIIB sequences is AAs 303-321 from HIVIIIB.
 CC (A) sequence is AAs 320-324 from HIVM and AAs 322-327 from HIVIIIB.
 CC Th = T helper cell determinant.
 CC B cell = B cell neutralising antibody determinant. A = additional
 CC HIV gp120 V3 loop sequences added to the original synthetic peptide
 CC (SP10) sequence to add an additional neutralising and CTL region
 CC to the HIV B cell determinant of the hybrid peptide. F (Immunogenic
 CC domain) sequence is AAs 519-530 from HIVIIIB.
 XX
 SQ Sequence 53 AA:

Query Match 63.7%; Score 130; DB 14; Length 53;
 Best Local Similarity 73.2%; Pred. No. 6.2e-09;
 Matches 30; Conservative 2; Mismatches 5; Indels 4; Gaps 2;

OY 1 KOIINMOWEYKAMYA--PISGQIR--RIORGPGRFAVTTI 37
 ||||| 1 : |||||
 DB 13 KqIINmwgevgkamyactrpnntkrkslrldrgprgratvltl 53

RESULT 13
 AAM16534
 ID AAM16534 standard; peptide: 53 AA.
 XX
 AC AAM16534;
 XX
 DT 14-JAN-1998 (first entry)
 XX
 DE Peptide (F-T1-SPL10(A)) comprising HIV antigenic determinant.
 XX
 KM Hydrophilic; antigenic determinant; HIV; envelope; glycoprotein;
 KM env; gp; recognition; B lymphocyte; type specific; antibody;
 KM vaccine; protection; immune response; infection; neutralisation.
 XX
 OS Human immunodeficiency virus.
 XX
 PN W09714436-A1.
 XX
 PD 24-APR-1997.
 XX
 PF 18-OCT-1996; 96WO-US16911.
 XX
 PR 09-FEB-1996; 96US-0599266.
 PR 20-OCT-1995; 95US-0546515.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Haynes BF, Parker TJ;
 XX
 DR WPI: 1997-244862/22.
 XX
 PT Synthetic human immunodeficiency virus vaccine - comprising
 PT hydrophilic peptide corresponding to at least 1 antigenic
 PT determinant of envelope glyco:protein recognised by B lymphocytes
 XX
 PS Disclosure: Page 18; 104pp; English.
 XX
 CC An essentially pure hydrophilic peptide, i.e. the present peptide,
 CC comprising at least 1 antigenic determinant of human
 CC immunodeficiency virus (HIV) envelope (env) glycoprotein (gp)
 CC recognised by B lymphocytes, when covalently linked to a carrier
 CC molecule induces the production of high titres of protective, type
 CC specific anti-HIV antibodies (Ab) in a mammal. The peptide can be
 CC used in vaccines for producing a protective immune response to HIV
 CC infection, while a HIV neutralising Ab can be induced in a primate
 CC by administering a composition comprising HIV env peptides that
 CC disrupt gp120/gp41 interactions.
 CC
 XX
 SQ Sequence 53 AA;

Query Match 63.7%; Score 130; DB 18; Length 53;
 Best Local Similarity 73.2%; Pred. No. 6.2e-09;
 Matches 30; Conservative 2; Mismatches 5; Indels 4; Gaps 2;

OY 1 KOIINMOWEYKAMYA--PISGQIR--RIORGPGRFAVTTI 37
 ||||| 1 : |||||
 DB 13 KqIINmwgevgkamyactrpnntkrkslrldrgprgratvltl 53

RESULT 14
 AAP94802
 ID AAP94802 standard; protein: 229 AA.
 XX

AC AAP94802;
 XX
 DT 22-JUN-1990 (first entry)
 XX
 DE PB1rf HIV fusion protein.
 XX
 KM HIV; AIDS; PB1rf fusion protein; HIV vaccine; ds.
 XX
 OS HIV.
 XX
 FH Key Location/Qualifiers
 FT Protein 31..156
 FT /label= HIV derived sequence
 XX
 PN EP306219-A.
 XX
 PD 08-MAR-1989.
 XX
 PF 25-AUG-1988; 88EP-0307889.
 XX
 PR 25-AUG-1988; 88EP-0307889.
 XX
 PA (REPL-) REPLIGEN CORP.
 XX
 PI Rusche JR, Putney SD, Javaherian K, Farley J, Grimalia R, Lynn D;
 PI Petro J, O'Keefe T;
 XX
 DR WPI: 1989-070387/10.
 DR N-PSDB; AAN90627.
 XX
 XX
 PT New HIV proteins and peptide(s) -
 PT used in diagnosis, prophylaxis or therapy of AIDS esp. for
 PT prepn. of vaccines against HIV infection.
 XX
 PS Claim 1; Table 4; 29pp; English.
 XX
 CC Protein derivative stimulates a lymphocyte proliferative response in
 CC HIV-infected humans, providing a means of diagnosis, protection and
 CC therapeutic value.
 CC
 XX
 SQ Sequence 229 AA;

Query Match 63.7%; Score 130; DB 10; Length 229;
 Best Local Similarity 68.4%; Pred. No. 2.4e-08;
 Matches 26; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

OY 1 KOIINMOWEYKAMYPAPISGQIRRIORGPGRFAVTTIG 38
 ||||| 1 : |||||
 DB 158 KqIIVmwgevgkamyappisgqikciscnltglllttdg 195

RESULT 15
 AAR33837
 ID AAR33837 standard; peptide: 24 AA.
 XX
 AC AAR33837;
 XX
 DT 13-JUL-1993 (first entry)
 XX
 DE Cluster peptide PCLUS3.
 XX
 KM Multideterminant; cluster; HIV; envelope protein; T-cell; mice; MHC;
 KM human; T lymphocyte; HLA; vaccine.
 XX
 OS Synthetic.
 XX
 PN W09304697-A.
 XX
 PD 18-MAR-1993.
 XX
 PF 31-AUG-1992; 92WO-US07422.
 XX

PR 29-AUG-1991; 91US-0751998.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
 XX
 XX
 PI Berzofsky JA;
 XX
 DR WPI; 1993-100657/12.
 XX
 PT Multi-determinant peptide antigens - stimulate T-helper response
 PT against HIV, for treating and diagnosing HIV infection
 XX
 PS Claim 7; Page 28; 37pp; English.
 XX
 CC The sequences given in AAR33835-40 are peptides which encompass multi-
 CC determinant clusters of HIV envelope protein that induce in vitro T-
 CC cell response in mice of multiple MHC type and in a population of HIV
 CC seropositive humans. These peptides stimulate helper T lymphocyte
 CC response to HIV in humans of many HLA types. They can be used for the
 CC diagnosis or prognosis of HIV, for the production of vaccines or for
 CC the therapeutic treatment of HIV infection.
 XX
 SQ Sequence 24 AA;

Query Match 62.3%; Score 127; DB 14; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.9e-09;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 ||||||||||||||||||||
 Db 1 KqIINmqevgKamYapIspqIr 24

Search completed: January 2, 2002, 09:57:22
 Job time: 32 sec

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OM protein - protein search, using sw model

Run on: January 2, 2002, 09:56:30 ; Search time 12.45 Seconds
(Without alignments)
70.492 Million cell updates/sec

Title: US-09-508-552-2

Perfect score: 204
Sequence: 1 KQIINMOEYGRAMYPITSGIRRIQKGPGRFVTGK 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	204	100.0	39	4 US-08-060-988A-2	Sequence 2, Appli
4	204	100.0	39	5 PCT-US94-05142-2	Sequence 2, Appli
5	171	83.8	39	2 US-08-455-625-28	Sequence 28, Appli
6	171	83.8	39	4 US-08-455-685-28	Sequence 28, Appli
7	171	83.8	39	4 US-08-060-988A-28	Sequence 28, Appli
8	171	83.8	39	5 PCT-US94-05142-28	Sequence 28, Appli
9	146.5	71.8	130	1 US-08-015-770B-8	Sequence 8, Appli
10	127	62.3	24	2 US-08-455-625-24	Sequence 24, Appli
11	127	62.3	24	2 US-08-407-252-3	Sequence 3, Appli
12	127	62.3	24	4 US-08-455-685-24	Sequence 24, Appli
13	127	62.3	24	4 US-08-060-988A-24	Sequence 24, Appli
14	127	62.3	24	5 PCT-US94-05142-24	Sequence 24, Appli
15	127	62.3	28	1 US-08-488-252-1	Sequence 1, Appli
16	127	62.3	28	2 US-08-448-603A-12	Sequence 12, Appli
17	127	62.3	28	3 US-09-134-075-12	Sequence 12, Appli
18	127	62.3	28	5 PCT-US92-0688-1	Sequence 1, Appli
19	127	62.3	181	5 PCT-US93-07805-1	Sequence 1, Appli
20	127	62.3	496	3 US-08-889-841B-12	Sequence 12, Appli
21	127	62.3	496	3 US-08-889-841B-16	Sequence 16, Appli
22	127	62.3	856	4 US-09-124-900-9	Sequence 9, Appli
23	127	62.3	863	3 US-08-463-210-11	Sequence 11, Appli
24	127	62.3	880	2 US-08-788-815-7	Sequence 7, Appli
25	127	62.3	880	2 US-09-157-963-7	Sequence 7, Appli
26	125	61.3	519	4 US-08-472-240A-18	Sequence 18, Appli
27	125	61.3	865	4 US-07-956-483-13	Sequence 13, Appli

28	125	61.3	887	4 US-08-472-240A-4	Sequence 4, Appli
29	123	60.3	27	2 US-08-493-235-34	Sequence 34, Appli
30	123	60.3	28	1 US-08-488-252-2	Sequence 2, Appli
31	123	60.3	28	1 US-08-488-252-3	Sequence 3, Appli
32	123	60.3	28	1 US-08-488-252-6	Sequence 6, Appli
33	123	60.3	28	1 US-08-488-252-7	Sequence 7, Appli
34	123	60.3	28	2 US-08-448-603A-4	Sequence 4, Appli
35	123	60.3	28	2 US-08-448-603A-5	Sequence 5, Appli
36	123	60.3	28	2 US-08-448-603A-10	Sequence 10, Appli
37	123	60.3	28	2 US-08-448-603A-11	Sequence 11, Appli
38	123	60.3	28	2 US-08-448-603A-13	Sequence 13, Appli
39	123	60.3	28	2 US-08-448-603A-15	Sequence 15, Appli
40	123	60.3	28	2 US-08-448-603A-21	Sequence 21, Appli
41	123	60.3	28	3 US-09-134-075-4	Sequence 4, Appli
42	123	60.3	28	3 US-09-134-075-5	Sequence 5, Appli
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44	123	60.3	28	3 US-09-134-075-11	Sequence 11, Appli
45	123	60.3	28	3 US-09-134-075-13	Sequence 13, Appli

ALIGNMENTS

RESULT 1
US-08-455-625-2
; Sequence 2, Application US/08455625
; Patent No. 5932218
; GENERAL INFORMATION:
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Ahlers, Jeffrey D.
; APPLICANT: Pendleton, C. D.
; APPLICANT: Nara, Peter
; APPLICANT: Shirai, Mutsunori
; TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT
; TITLE OF INVENTION: ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T
; TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,625
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,988
; FILING DATE: 14-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 1173-434P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..39

OTHER INFORMATION: /label= peptide
OTHER INFORMATION: /note= "pctus 3-18/p181i1B peptide, see Table 1"
US-08-455-625-2

Query Match 100.0%; Score 204; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.7e-22;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIIMMOEVGKAMYPAPISQIRIRIOGPGRAFTVIGK 39
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Db 1 KOIIMMOEVGKAMYPAPISQIRIRIOGPGRAFTVIGK 39

RESULT 2

US-08-455-685-2
Sequence 2, Application US/08455685
Patent No. 6214347
GENERAL INFORMATION:
APPLICANT: Berzofsky, Jay A.
APPLICANT: Ahlers, Jeffrey D.
APPLICANT: Pendleton, C. David
APPLICANT: Nara, Peter
APPLICANT: Shirai, Mutsunori
TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES THAT ELICIT
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND
TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,685
FILING DATE: 31-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/060,988
FILING DATE: 14-MAY-1993
APPLICATION NUMBER: 07/847,311
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/751,998
FILING DATE: 29-AUG-1991
APPLICATION NUMBER: 07/148,692
FILING DATE: 26-JAN-1988
ATTORNEY/AGENT INFORMATION:
NAME: Beattie, Ingrid A.
REGISTRATION NUMBER: P-42,306
REFERENCE/DOCKET NUMBER: 08830/022003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-455-685-2

Query Match 100.0%; Score 204; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.7e-22;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 1 KOIIMMOEVGKAMYPAPISQIRIRIOGPGRAFTVIGK 39

RESULT 3

US-08-060-988A-2
Sequence 2, Application US/08060988A
Patent No. 6294322
GENERAL INFORMATION:
APPLICANT: Berzofsky, Jay A.
APPLICANT: Ahlers, Jeffrey D.
APPLICANT: Pendleton, C. David
APPLICANT: Nara, Peter
APPLICANT: Shirai, Mutsunori
TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES
TITLE OF INVENTION: THAT ELICIT
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND
TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/060,988A
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/847,311
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/751,998
FILING DATE: 29-AUG-1991
APPLICATION NUMBER: 07/148,692
FILING DATE: 26-JAN-1988
ATTORNEY/AGENT INFORMATION:
NAME: Beattie, Ingrid A.
REGISTRATION NUMBER: P-42,306
REFERENCE/DOCKET NUMBER: 08830/022001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-060-988A-2

Query Match 100.0%; Score 204; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.7e-22;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 1 KOIIMMOEVGKAMYPAPISQIRIRIOGPGRAFTVIGK 39

RESULT 4

PCT-US94-05142-2
Sequence 2, Application PC/TUS9405142
GENERAL INFORMATION:
APPLICANT:

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: TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT
: TITLE OF INVENTION: ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T
: TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Birch, Stewart, Kolasch & Birch
: STREET: P.O. Box 747
: CITY: Falls Church
: STATE: Virginia
: COUNTRY: USA
: ZIP: 22040-0747
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/05142
: FILING DATE: 13-MAY-1994
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/060,988
: FILING DATE: 14-MAY-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Svensson, Leonard R.
: REGISTRATION NUMBER: 30330
: REFERENCE/DOCKET NUMBER: 1173-434P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-205-8000
: TELEFAX: 703-205-8050
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 39 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: 1..39
: OTHER INFORMATION: /label= peptide
: OTHER INFORMATION: /note= "pclus 3-18/p18ITB peptide, see Table 1"
: PCT-US94-05142-2

Query Match 100.0%; Score 204; DB 5; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.7e-22;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOIIMMOEVGKAMVAPISGQIRIRIQGPGRAFTICK 39
DB 1 KOIIMMOEVGKAMVAPISGQIRIRIQGPGRAFTICK 39

RESULT 5
US-08-455-625-28
: Sequence 28, Application US/08455625
: Patent No. 5932218
: GENERAL INFORMATION:
: APPLICANT: Berzofsky, Jay A.
: APPLICANT: Ahlers, Jeffrey D.
: APPLICANT: Pendleton, C. D.
: APPLICANT: Nara, Peter
: APPLICANT: Shirai, Mutsunori
: TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT
: TITLE OF INVENTION: ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T
: TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Birch, Stewart, Kolasch & Birch
: STREET: P.O. Box 747
: CITY: Falls Church
: STATE: Virginia
```

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: COUNTRY: USA
: ZIP: 22040-0747
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/455,625
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/060,988
: FILING DATE: 14-MAY-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Svensson, Leonard R.
: REGISTRATION NUMBER: 30330
: REFERENCE/DOCKET NUMBER: 1173-434P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-205-8000
: TELEFAX: 703-205-8050
: INFORMATION FOR SEQ ID NO: 28:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 39 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: 1..39
: OTHER INFORMATION: /label= peptide
: OTHER INFORMATION: /note= "pclus3-18MN peptide, see Table VI"
: US-08-455-625-28

Query Match 83.8%; Score 171; DB 2; Length 39;
Best Local Similarity 91.7%; Pred. No. 2.3e-17;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KOIIMMOEVGKAMVAPISGQIRIRIQGPGRAFT 36
DB 1 KOIIMMOEVGKAMVAPISGQIRIRIHGPGRAFT 36

RESULT 6
US-08-455-685-28
: Sequence 28, Application US/08455685
: Patent No. 6214347
: GENERAL INFORMATION:
: APPLICANT: Berzofsky, Jay A.
: APPLICANT: Ahlers, Jeffrey D.
: APPLICANT: Pendleton, C. David
: APPLICANT: Nara, Peter
: APPLICANT: Shirai, Mutsunori
: TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES THAT ELICIT
: TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND
: TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1
: NUMBER OF SEQUENCES: 40
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: IBM compatible
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/455,685
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FILED DATE: 31-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/060,988
FILING DATE: 14-MAY-1993
APPLICATION NUMBER: 07/847,311
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/751,998
FILING DATE: 29-AUG-1991
APPLICATION NUMBER: 07/148,692
FILING DATE: 26-JAN-1988
ATTORNEY/AGENT INFORMATION:
NAME: Beattie, Ingrid A.
REGISTRATION NUMBER: P-42,306
REFERENCE/DOCKET NUMBER: 08830/022003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-455-685-28

Query Match 83.8%; Score 171; DB 4; Length 39;
Best Local Similarity 91.7%; Pred. No. 2.3e-17;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KOIINMDEVGKAMTAPISGQIRIHIGPGRFVT 36
DB 1 KOIINMDEVGKAMTAPISGQIRIHIGPGRFVT 36

RESULT 7
US-08-060-988A-28
Sequence 28, Application US/08060988A
Patent No. 6294322
GENERAL INFORMATION:
APPLICANT: Berzofsky, Jay A.
APPLICANT: Ahlers, Jeffrey D.
APPLICANT: Pendleton, C. David
APPLICANT: Nara, Peter
APPLICANT: Shital, Mutsunori
TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES
TITLE OF INVENTION: THAT ELICIT
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND
TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/060,988A
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/847,311
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/751,998
FILING DATE: 29-AUG-1991
APPLICATION NUMBER: 07/148,692
FILING DATE: 26-JAN-1988

ATTORNEY/AGENT INFORMATION:
NAME: Beattie, Ingrid A.
REGISTRATION NUMBER: P-42,306
REFERENCE/DOCKET NUMBER: 08830/022001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-060-988A-28

Query Match 83.8%; Score 171; DB 4; Length 39;
Best Local Similarity 91.7%; Pred. No. 2.3e-17;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KOIINMDEVGKAMTAPISGQIRIHIGPGRFVT 36
DB 1 KOIINMDEVGKAMTAPISGQIRIHIGPGRFVT 36

RESULT 8
PCT-US94-05142-28
Sequence 28, Application PC/TUS9405142
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT
TITLE OF INVENTION: ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T
NUMBER OF INVENTION: LYMPHOCYTES AGAINST HIV
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05142
FILING DATE: 13-MAY-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,988
FILING DATE: 14-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30330
REFERENCE/DOCKET NUMBER: 1173-434P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..39
OTHER INFORMATION: /label= peptide
OTHER INFORMATION: /note= "pctus3-18MN peptide, see Table VI"

PCT-US94-05142-28

Query Match 83.8%; Score 171; DB 5; Length 39;
Best Local Similarity 91.7%; Pred. No. 2,3e-17;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KOIIMMOEVGKAMYAPISGQIRIRQRPGRFYT 36
DB 1 KOIIMMOEVGKAMYAPISGQIRIRHIGPGRFYT 36

RESULT 9

US-08-015-770B-8
Sequence 8, Application US/08015770B
Patent No. 5683695

GENERAL INFORMATION:

APPLICANT: Shen, De Fen

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: Production of recombinant proteins
TITLE OF INVENTION: containing multiple antigenic determinants linked by

TITLE OF INVENTION: flexible domains

NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:

ADDRESS: United Biomedical, Inc.

STREET: 25 Davids Drive

CITY: Hauppauge

STATE: NY

COUNTRY: USA

ZIP: 11788

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/015,770B

FILING DATE: 10-FEB-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Wilson, M. Lisa

REGISTRATION NUMBER: 34,045

REFERENCE/DOCKET NUMBER: 2002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516)273-1717

TELEFAX: (516)273-2828

INFORMATION FOR SEQ. ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 150 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-015-770B-8

Query Match 71.8%; Score 146.5; DB 1; Length 150;
Best Local Similarity 68.9%; Pred. No. 2,9e-13;
Matches 31; Conservative 1; Mismatches 4; Indels 9; Gaps 1;

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DB 4 KOIIMMOEVGKAMYAPISGQIRCDPPDPKRAHIGGRFYT 48

RESULT 10

US-08-455-625-24
Sequence 24, Application US/08455625
Patent No. 5932218

GENERAL INFORMATION:

APPLICANT: Berzofsky, Jay A.

APPLICANT: Ahlers, Jeffrey D.

APPLICANT: Pendleton, C. D.

APPLICANT: Nara, Peter

APPLICANT: Nara, Peter

APPLICANT: Nara, Peter

APPLICANT: Shirai, Mutsunori
TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT
TITLE OF INVENTION: ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T
TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:

ADDRESS: Birch, Stewart, Kolasch & Birch

STREET: P.O. Box 747

CITY: Falls Church

STATE: Virginia

COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,625

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/060,988

FILING DATE: 14-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Svensson, Leonard R.

REGISTRATION NUMBER: 30330

REFERENCE/DOCKET NUMBER: 1173-434P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-205-8000

TELEFAX: 703-205-8050

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..24

OTHER INFORMATION:

/note="pclus3 peptide"

US-08-455-625-24

Query Match 62.3%; Score 127; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No 1,9e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOIIMMOEVGKAMYAPISGQIR 24
DB 1 KOIIMMOEVGKAMYAPISGQIR 24

RESULT 11

US-08-407-252-3
Sequence 3, Application US/08407252
Patent No. 5936074

GENERAL INFORMATION:

APPLICANT: Berzofsky, Jay A

TITLE OF INVENTION: Multideterminant Peptide Antigens that

TITLE OF INVENTION: Stimulate Helper T Lymphocyte Response to HIV in a Range

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Crew

STREET: Two Embarcadero Center, 8th Fl.

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/407,252
FILING DATE: 20-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,730
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/751,998
FILING DATE: 29-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/492,318
FILING DATE: 28-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/148,692
FILING DATE: 26-JAN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/222,684
FILING DATE: 21-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: KING, JEFFREY J.
REGISTRATION NUMBER: 38515
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 206-623-6793
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: HIV-1
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..25
OTHER INFORMATION: /label= peptide
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FEATURE:
NAME/KEY: Peptide
LOCATION: 1..16
OTHER INFORMATION: /label= peptide
OTHER INFORMATION: /note= "peptide hp-26 in table 2"
FEATURE:
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LOCATION: 5..19
OTHER INFORMATION: /label= peptide
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FEATURE:
NAME/KEY: Peptide
LOCATION: 10..24
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OTHER INFORMATION: /note= "peptide hp-29 in table 2"
PUBLICATION INFORMATION:
DOCUMENT NUMBER: US 5,030,449
FILING DATE: 21-JUL-1988
PUBLICATION DATE: 09-JUL-1991
RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 TO 20
PUBLICATION INFORMATION:
DOCUMENT NUMBER: US 07/148,692
FILING DATE: 26-JAN-1988
RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 TO 20
US-08-407-252-3

Query Match 62.3%, Score 127, DB 2, Length 24;
Best Local Similarity 100.0%, Pred. No. 1.9e-11;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 KOIINMGEVGMKAMVAPPISQIR 24
RESULT 12
US-08-455-685-24
Sequence 24, Application US/08455685
Patent No 6214347
GENERAL INFORMATION:
APPLICANT: Beizolsky, Jay A.
APPLICANT: Ahlers, Jeffrey D.
APPLICANT: Pendleton, C. David
APPLICANT: Nara, Peter
APPLICANT: Shirai, Mutsunori
TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES THAT ELICIT
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND
TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,685
FILING DATE: 31-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/060,988
FILING DATE: 14-MAY-1993
APPLICATION NUMBER: 07/847,311
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/751,998
FILING DATE: 29-AUG-1991
APPLICATION NUMBER: 07/148,692
FILING DATE: 26-JAN-1988
ATTORNEY/AGENT INFORMATION:
NAME: Beattie, Ingrid A.
REGISTRATION NUMBER: P-42,306
REFERENCE/DOCKET NUMBER: 08830/022003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-455-685-24

Query Match 62.3%, Score 127, DB 4, Length 24;
Best Local Similarity 100.0%, Pred. No. 1.9e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOIINMGEVGMKAMVAPPISQIR 24
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DB 1 KOIINMGEVGMKAMVAPPISQIR 24

RESULT 13
US-08-060-988A-24

Wed Jan 2 10:00:38 2002

us-09-508-552-2.rai

Page 8

Search completed: January 2, 2002, 09:56:51
Job time: 21 sec

FILED DATE: 424
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08\326,676
FILING DATE: 07-Jun-1995
APPLICATION NUMBER: 07\726,605
FILING DATE: 09-Jul-1991
APPLICATION NUMBER: 07\663,262
FILING DATE: 01-Mar-1991
APPLICATION NUMBER: 07\155,321
FILING DATE: 12-Feb-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria C. H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4004 US4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-488-252-1

Query Match 62.3%; Score 127; DB 1; Length 28;
Best local similarity 100.0%; Pred. No. 2.2e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KÖLINMÖEVGKAMTAPDISQIR 24
|||||
Db 4 KÖLINMÖEVGKAMTAPDISQIR 27

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 2, 2002, 09:56:30 ; Search time 13.57 Seconds
(without alignments)
218.925 Million cell updates/sec

Title: US-09-508-552-2

Perfect score: 204
Sequence: 1 KQIINMMEVGKAMVAPISGQIRIRIGRPGRAFTIGK 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	62.3	851	2 S33985	env polypeptide -
2	127	62.3	856	1 VCLJH3	env polypeptide pr
3	123	60.3	506	2 A40218	envelope glycoprote
4	123	60.3	854	2 S13288	env protein - huma
5	123	60.3	856	1 VCLJVL	env polypeptide pr
6	123	60.3	859	1 VCLJMN	env polypeptide pr
7	123	60.3	861	1 VCLJLV	env polypeptide pr
8	122	59.8	290	2 S25940	env protein - huma
9	122	59.8	297	2 S60538	envelope polypepte
10	122	59.8	443	2 C41621	env polypeptide p
11	122	59.8	843	1 H44001	env polypeptide pr
12	122	59.8	847	2 T09448	envelope glycoprote
13	121	59.3	445	2 A41621	env polypeptide M
14	121	59.3	729	1 VCLJRX	env polypeptide pr
15	121	59.3	861	1 VCLJKB	env polypeptide pr
16	119	58.3	852	1 VCLJBR	env protein - huma
17	118	57.8	847	2 S13289	env polypeptide pr
18	118	57.8	855	1 VCLJAJ	envelope glycoprote
19	116	56.9	852	2 T12016	env polypeptide pr
20	116	56.9	856	1 VCLJ3W	env polypeptide pr
21	116	56.9	861	1 VCLJSC	env polypeptide pr
22	114	55.9	454	2 B41621	envelope polypepte
23	111	54.4	853	1 S54384	env polypeptide pr
24	111	54.4	855	1 VCLJZR	envelope polypepte
25	110	53.9	300	2 S60522	envelope polypepte
26	109	53.4	294	2 S60525	envelope polypepte
27	109	53.4	300	2 S60547	envelope polypepte
28	109	53.4	300	2 S60546	envelope polypepte
29	109	53.4	301	2 S60548	envelope polypepte

30	106	52.0	294	2 S60545	envelope polypepte
31	106	52.0	294	2 S60522	envelope polypepte
32	106	52.0	301	2 S60532	envelope polypepte
33	106	52.0	301	2 S60531	envelope polypepte
34	105	51.5	303	2 S60550	envelope polypepte
35	105	51.5	303	2 S60549	envelope polypepte
36	104	51.0	299	2 S60529	envelope polypepte
37	104	51.0	299	2 S60552	envelope polypepte
38	104	51.0	299	2 S60521	envelope polypepte
39	104	51.0	299	2 S60551	envelope polypepte
40	104	51.0	299	2 S60523	envelope polypepte
41	104	51.0	299	2 S60553	envelope polypepte
42	104	51.0	299	2 S60554	env polypeptide pr
43	104	51.0	495	2 S31493	env polypeptide pr
44	104	51.0	846	1 VCLJND	env polypeptide pr
45	104	51.0	856	1 A44963	env polypeptide pr

ALIGNMENTS

RESULT 1

S33985 env polypeptide - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1 HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999

C:Accession: S33985

R:Carlini, F.
submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33985

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-851 <CAR>

A:Cross-references: EMBL:211530; NID:960192; PIDN:CAA77628.1; PID:960199

C:Superfamily: type E retrovirus env polypeptide

Query Match 62.3%; Score 127; DB 2; Length 851;

Best local Similarity 100.0%; Pred. No. 2; 1e-09;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KQIINMMEVGKAMVAPISGQIR 24

DB 416 KQIINMMEVGKAMVAPISGQIR 439

RESULT 2

VCLJH3 env polypeptide precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH

N:Alternate names: coat polypeptide

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

C:Accession: A03973

R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; D

ubneger, J.A.; Pappas, T.S.; Chirgwin, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.

Nature 313, 277-284, 1985

A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.

A:Reference number: A93353; M0ID:85111123

A:Accession: A03973

A:Molecule type: DNA

A:Residues: 1-856 <RAT>

A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:9326383; PIDN:AAA

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; poly

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-511/Product: exterior membrane glycoprotein #status predicted <TM>

F:512-856/Product: transmembrane glycoprotein #status predicted <TM>

F:88-136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,

F:611,616,625,637,674,750,816/Binding site: carbohydrate (asn) (covalent) #status pre

Query Match 62.3%; Score 127; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOIIMMOEVBKAMYAPISQIR 24
DB 421 KOIIMMOEVBKAMYAPISQIR 444

RESULT 3

env polyp protein gp120 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Apr-1995
C:Accession: A40218
R:Turner, S.; Tizard, R.; DeMarinis, J.; Pepinsky, R.B.; Zullo, J.; Schooley, R.; Fisher
Proc. Natl. Acad. Sci. U.S.A. 89, 1335-1339, 1992
A:Title: Resistance of primary isolates of human immunodeficiency virus type 1 to neutra
A:Reference number: A40218; MUID:92159044
A:Accession: A40218
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-506 <TUR>
A:Experimental source: isolate P17
A:Note: sequence extracted from NCBI backbone (NCBIF:82240)
C:Superfamily: type E retrovirus env polyp protein
C:Keywords: glycoprotein

Query Match 60.3%; Score 123; DB 2; Length 506;
Best Local Similarity 95.8%; Pred. No. 4.3e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOIIMMOEVBKAMYAPISQIR 24
DB 414 KOIIMMOEVBKAMYAPISQIR 437

RESULT 4

env polyp protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S13288
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A:Reference number: S13288; MUID:91043044
A:Accession: S13288
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-854 <OBR>
C:Superfamily: type E retrovirus env polyp protein

Query Match 60.3%; Score 123; DB 2; Length 854;
Best Local Similarity 95.8%; Pred. No. 7.4e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOIIMMOEVBKAMYAPISQIR 24
DB 419 KOIIMMOEVBKAMYAPISQIR 442

RESULT 5

env polyp protein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polyp protein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

C:Accession: A03974
R:Mesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retr
A:Reference number: A93355; MUID:85111157
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <MUE>
A:Cross-References: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559
C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyp protein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,
F:611,616,625,637,674,750,816/Binding site: carbohydrate (asn) (covalent) #status pre

Query Match 60.3%; Score 123; DB 1; Length 856;
Best Local Similarity 95.8%; Pred. No. 7.4e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOIIMMOEVBKAMYAPISQIR 24
DB 421 KOIIMMOEVBKAMYAPISQIR 444

RESULT 6

env polyp protein precursor - human immunodeficiency virus type 1 (isolate MN)
N:Alternate names: coat polyp protein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C:Accession: A28922
R:Gungo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-
Virolgy 164, 531-536, 1988
A:Title: Envelope sequences of two new United States HIV-1 isolates.
A:Reference number: A28922; MUID:88219542
A:Accession: A28922
A:Molecule type: DNA
A:Residues: 1-859 <GUR>
C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyp protein

C:Keywords: capsid protein; coat protein; glycoprotein; polyp protein; transmembrane pr
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-859/Product: env polyp protein #status predicted <EPP>
F:87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,

Query Match 60.3%; Score 123; DB 1; Length 859;
Best Local Similarity 95.8%; Pred. No. 7.4e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOIIMMOEVBKAMYAPISQIR 24
DB 424 KOIIMMOEVBKAMYAPISQIR 447

RESULT 7

env polyp protein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyp protein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Allizon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.

A:Reference number: A90866; MUID:85099333
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <MA1>
A:Cross-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-516/Product: exterior membrane glycoprotein #status predicted <TM>
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>
F:88-136,141,146,161,165,191,202,246,267,281,294,300,306,337,344,361,391,397,402,411
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 60.3%; Score 123; DB 1; Length 861;
Best Local Similarity 95.8%; Pred. No. 7.4e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOIINMGEVGRKAMYAPPISQIR 24
DB 426 KOIINMGEVGRKAMYAPPISQIR 449

RESULT 8
S25940
env protein - human immunodeficiency virus type 1 (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 22-Nov-1993 #sequence_revision 30-Jan-1998 #text_change 26-Aug-1999
C:Accession: S25940
R:Guo, H.G.; Chermann, J.C.; Waters, D.; Hall, L.; Louie, A.; Gallo, R.C.; Streicher, H.
Nature 349, 745-746, 1991
A:Title: Sequence analysis of original HIV-1.
A:Reference number: S25937; MUID:91156044
A:Accession: S25940
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-290 <GUO>
A:Cross-references: EMBL:X57449; NID:g60208; PIDN:CAA0695.1; PID:g60209
A:Experimental source: strain JBB
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1991
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein

Query Match 59.8%; Score 122; DB 2; Length 290;
Best Local Similarity 95.8%; Pred. No. 3.3e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOIINMGEVGRKAMYAPPISQIR 24
DB 145 KOIINMGEVGRKAMYAPPISQIR 168

RESULT 9
S60538
envelope polyprotein gp41 - human immunodeficiency virus type 1 (isolate CI-22-3 and oth
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate CI-22-3; isolate CI-22-6; isolate CI-22-10
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
C:Accession: S60538; S60539; S60540
R:Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Franssen, K.; Motte, J.;
AIDS 8, 21-26, 1994
A:Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cote d
A:Reference number: S60521; MUID:94280700
A:Accession: S60538
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-297 <JAN>
A:Cross-references: EMBL:X72040; NID:g468655; PIDN:CAA50925.1; PID:g468656

A:Experimental source: isolate CI-22-3
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
A:Accession: S60539
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-297 <JAN>
A:Cross-references: EMBL:X72041; NID:g468657; PIDN:CAA50924.1; PID:g468658
A:Experimental source: isolate CI-22-6
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
A:Accession: S60540
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-297 <JAN>
A:Cross-references: EMBL:X72042; NID:g468659; PIDN:CAA50925.1; PID:g468660
A:Experimental source: isolate CI-22-10
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; glycoprotein; immunodeficiency; polyprotein

Query Match 59.8%; Score 122; DB 2; Length 297;
Best Local Similarity 95.8%; Pred. No. 3.4e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOIINMGEVGRKAMYAPPISQIR 24
DB 148 KOIINMGEVGRKAMYAPPISQIR 171

RESULT 10
C41621
env polyprotein P - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polyprotein
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: C41621
R:Burger, H.; Welser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversi
A:Reference number: A41621; MUID:92107924
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: GB:M77230; NID:g328631; PIDN:AAB03792.1; PID:g555015
A:Note: this virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <TM>
F:424-443/Domain: transmembrane #status predicted <TM>
F:9,23,36,46,76,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:
F:9,23,36,46,76,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:

Query Match 59.8%; Score 122; DB 2; Length 443;
Best Local Similarity 95.8%; Pred. No. 5.1e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOIINMGEVGRKAMYAPPISQIR 24
DB 161 KOIINMGEVGRKAMYAPPISQIR 184

RESULT 11
H44001
env polyprotein precursor - human immunodeficiency virus type 1 (strain YU-2)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Sep-1994
C:Accession: H44001
R:Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992
A:Title: Complete nucleotide sequence, genome organization, and biological properties of
A:Reference number: A44001; MUID:93021387
A:Accession: H44001
A:Molecule type: DNA
A:Residues: 1-843 <LiY>
A:Cross-references: GB:M3258
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:19-35/Region: hydrophobic
F:30-489/Product: coat protein gp120 #status predicted <GP1>
F:490-843/Product: coat protein gp41 #status predicted <GP2>
F:499-515/Region: hydrophobic
F:673-689/Region: hydrophobic
F:738-755/Domain: transmembrane #status predicted <TMN>
F:87,129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,433

Query Match 59.8%; Score 122; DB 1; Length 843;
Best Local Similarity 95.8%; Pred. No. 1e-08;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQIINMGEVGMKAMYAPPIRQIR 24
|||:|||||
DB 408 KQIINMGEVGMKAMYAPPIRQIR 431

RESULT 12
T09448
envelope glycoprotein - human immunodeficiency virus type 1 (strain JFRL)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
C:Accession: T09448
R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,
submitted to the EMBL Data Library, July 1996
A:Reference number: Z16673
A:Accession: T09448
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-847 <PAN>
A:Cross-references: EMBL:U63632; NID:q1465777; PID:q1465781
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein

Query Match 59.8%; Score 122; DB 2; Length 847;
Best Local Similarity 95.8%; Pred. No. 1e-08;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQIINMGEVGMKAMYAPPIRQIR 24
|||:|||||
DB 412 KQIINMGEVGMKAMYAPPIRQIR 435

RESULT 13
A41621
env polyprotein M - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polyprotein
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: A41621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924
A:Accession: A41621
A:Molecule type: DNA
A:Residues: 1-445 <BUR>
A:Cross-references: GB:M77228; NID:9328627; PID:NAB03790.1; PID:9555013
A:Note: this virus was isolated from the mother
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; poly
F:1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:426-445/Domain: transmembrane #status predicted <TMN>
F:9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding s1

Query Match 59.3%; Score 121; DB 2; Length 445;
Best Local Similarity 91.7%; Pred. No. 7.1e-09;
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQIINMGEVGMKAMYAPPIRQIR 24
|||:|||||
DB 163 KQIINMGEVGMKAMYAPPIRQIR 186

RESULT 14
VCLJKB
env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp32
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Mar-1996
C:Accession: B42995
R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
Virology 189, 534-546, 1992
A:Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncat
A:Reference number: A42995; MUID:92351552
A:Accession: B42995
A:Molecule type: mRNA
A:Residues: 1-729 <SHI>
A:Cross-references: GB:S41266; GB:D01206
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-689/Domain: extracellular #status predicted <EXT>
F:1-33/Domain: signal sequence #status predicted <SIG>
F:17-33/Region: hydrophobic #status predicted
F:34-517/Product: coat protein gp120 #status predicted <CP1>
F:514-517/Region: cleavage processing #status predicted
F:518-729/Product: coat protein gp32 #status predicted <CP2>
F:518-534/Region: hydrophobic #status predicted
F:690-711/Domain: transmembrane #status predicted <TMN>
F:712-729/Domain: intracellular #status predicted <INT>
F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,

Query Match 59.3%; Score 121; DB 1; Length 729;
Best Local Similarity 91.7%; Pred. No. 1.2e-08;
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQIINMGEVGMKAMYAPPIRQIR 24
|||:|||||
DB 422 KQIINMGEVGMKAMYAPPIRQIR 445

RESULT 15
VCLJKB
env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp41)
N:Alternate names: coat polyprotein

N:Contains: coat protein gp120; coat protein gp41
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Note: host Homo sapiens (man)
 C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 01-Mar-1996
 C:Accession: A42995
 R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
 Virology 189, 534-546, 1992
 A:title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated
 A:Reference number: A42995; MOID:92351552
 A:Accession: A42995
 A:Molecule type: mRNA
 A:Residues: 1-861 <SH1>
 A:Cross-references: GB:S41266; GB:D01206
 C:Genetics:
 A:Gene: env
 C:Superfamily: type E retrovirus env polyprotein
 C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
 F:1-689/Domain: extracellular #status predicted <EXT>
 F:1-33/Domain: signal sequence #status predicted <SIG>
 F:17-33/Region: hydrophobic #status predicted
 F:34-517/Product: coat protein gp120 #status predicted <CP1>
 F:514-517/Region: cleavage processing #status predicted
 F:518-861/Product: coat protein gp41 #status predicted <CP2>
 F:518-534/Region: hydrophobic #status predicted
 F:680-711/Domain: transmembrane #status predicted <TM1>
 F:712-861/Domain: intracellular #status predicted <INT>
 F:756-772/Region: hydrophobic #status predicted
 F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414

Query Match 59.38; Score 121; DB 1; Length 861;
 Best Local Similarity 91.78; Pred. No. 1.4e-08;
 Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOIINMGEVGKAMYAPPISQIR 24
 |||:||||||| |||
 Db 422 KOIYNMGEVGKAMYAPPISQIR 445

Search completed: January 2, 2002, 09:57:42
 Job time: 72 sec


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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;
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Query Match 62.3%; Score 127; DB 1; Length 851;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KOIINMOEVGKAMYAPISGOIR 24
|||||
Db 416 KOIINMOEVGKAMYAPISGOIR 439

ENV_HV1B1 STANDARD; PRT; 856 AA.
ID ENV_HV1B1
AC P03375;

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).
GN ENV.

OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11678;
[1]
SEQUENCE FROM N.A.

RP MEDLINE=8511123; PubMed=2578615.

RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,

RA Josephs S.F., Doran E.R., Ratajski J.A., Whitehorn E.A.,

RA Baumeshter K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,

RA Lautenberger J.A., Pappas T.S., Ghayeb J., Chang N.T., Gallo R.C.,

RA Wong-Staal F.;
"Complete nucleotide sequence of the AIDS virus, HTLV-III.";

RL Nature 313:277-284(1985).

RN [2]
DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.

RA MEDLINE=90285159; PubMed=2355006;

RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,

RA Gregory T.J.;
"Assignment of intrachain disulfide bonds and characterization of

RT potential glycosylation sites of the type 1 recombinant human

RT immunodeficiency virus envelope glycoprotein (gp120) expressed in

RT Chinese hamster ovary cells";
J. Biol. Chem. 265:10373-10382(1990).

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or send an email to license@isb-sib.ch).

DR EMBL: M15654; AAA44205.1; -.
DR PIR: A03973; VCLJH3.
DR HIV; M15654; ENV\$H102.
DR Interpro; IPR000328; Env_GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.

FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 625 625
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97224 MW; 0BPF1A18931BB27 CRC64;

Query Match 62.3%; Score 127; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KOIINMOEVGKAMYAPISGOIR 24
|||||
Db 421 KOIINMOEVGKAMYAPISGOIR 444

ENV_HV1LW

[illegible]

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FT CARBOHYD 626 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 856 AA; 96938 MW; 0C241332CF766687 CMC64;

Query Match 62.3%; Score 127; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 3..3e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOIINMOEVGKAMYAPISGOIR 24
Db 421 KOIINMOEVGKAMYAPISGOIR 444
|||||

RESULT 4
ENV_HYLOX STANDARD; PRT; 855 AA.
ID ENV_HYLOX
AC P20886;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11699;
RX MEDLINE=90148544; Pubmed=2559749;
RP SEQUENCE FROM N.A.
RA Huett T., Dazza M.C., Brun-Yezinet F., Roelants G.E., Nahn-Hobson S.;
RT "A highly defective HIV-1 strain isolated from a healthy Gabonese
RT individual presenting an atypical western blot.";
RL AIDS 3:707-715(1989).
-1 MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A
HEALTHY GABONESE INDIVIDUAL.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, M26727; AAA83397.1; -.
DR HIV; M26727; ENVSOVI.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
KW SIGNAL 1 29
FT CHAIN 30 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 510 855 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 210 BY SIMILARITY.
FT DISULFID 125 201 BY SIMILARITY.
FT DISULFID 130 162 BY SIMILARITY.
FT DISULFID 223 252 BY SIMILARITY.
FT DISULFID 301 335 BY SIMILARITY.
FT DISULFID 381 442 BY SIMILARITY.
FT DISULFID 388 415 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).

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Query Match	Best Local Similarity	Score 125;	DB 1;	Length 865;
Matches 24;	Conservative %;	2;	Mismatches 5;	Indels 0;
Gaps 0;				
Qy 1 KOIINMGEVGKAMYAPISQIRIQSGPG 31				
Db 428 KOIVNMGEVGKAMYAPISQIRIQSGPG 458				
RESULT 6				
ENV_HV1JR	STANDARD;	PRT;	848 AA.	
AC P20871;				
DT 01-FEB-1991 (Rel. 17, Created)				
DT 01-FEB-1991 (Rel. 17, Last sequence update)				
DT 15-JUL-1999 (Rel. 38, Last annotation update)				
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTRAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].				
GN ENV.				
OS Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).				
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.				
OX NCBI_Taxid=11688;				
NP [1]				
SEQUENCE FROM N.A.				

DR HIV; K03455; ENVSHXB2.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 624 624
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97212 MM; 6FBA16AFB5107FED CRC64;

Query Match 60.3%; Score 123; DB 1; Length 856;
Best Local Similarity 95.8%; Pred. No. 1.2e-09;
Matches 23; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMDEVKAMYPAPISQIR 24
DB 421 KOIINMDEVKAMYPAPISQIR 444

RESULT 10
ENV_HV1H3 STANDARD: PRT; 856 AA.
AC P04624;
DT 13-AUG-1987 (rel. 05. Created)
DT 01-FEB-1996 (rel. 33. Last sequence update)
DT 15-JUL-1999 (rel. 38. Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
DB GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).

CC Viruses; Retrovirus; Retroviridae; Lentivirus.
OX NCBI_TaxID=11707;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85228248; PubMed=2988795;
RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,
RT Shaw G.M., Wong-Staal F., Reddy E.P.;
RT "HIV-III env gene products synthesized in E. coli are recognized by
RU antibodies present in the sera of AIDS patients.";
RL Cell 41:979-986(1985).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M14100; AAA44679.1; -;
DR HIV; M14100; ENVSHXB3.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
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FT CARBOHYD 397 397
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FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 624 624
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97188 MM; 3373C6BB84C1AFC CRC64;

Query Match 60.3%; Score 123; DB 1; Length 856;

Best Local Similarity 95.8%; Pred. No. 1.2e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOIINMOWEYKAMYAPPISQIR 24
DB 421 KOIINMOWEYKAMYAPPISQIR 444

RESULT 11

ENV_HV1MN STANDARD: PRT; 856 AA.

AC P05877; 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPROTEIN GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC Viruses; Retrovirda; Retroviridae; Lentivirus.
OX NCBI_TaxId=11696;

RN [1]
RP MEDLINE=88219542; Pubmed=3369091;
RA Guirgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrel K., Mong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates."
RL Virology 164:531-536(1988)
CC -1 MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
PATIENT IN 1984.

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DR EMBL: M17449; AAA44857.1; -
DR PIR: A28922; VCLJMN.
DR HIV: M17449; ENVSMN.
DR InterPro: IPR000328; Env-GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.

KW AIDS; Coat protein; Polypotein; Glycoprotein; Transmembrane;
Signal.

FT SIGNAL 1 29
FT CHAIN 30 513
FT CHAIN 514 856
FT DISULFID 53 73
FT DISULFID 118 210
FT DISULFID 125 201
FT DISULFID 130 162
FT DISULFID 223 252
FT DISULFID 233 244
FT DISULFID 301 335
FT DISULFID 381 445
FT DISULFID 388 418
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 135 135
FT CARBOHYD 140 140
FT CARBOHYD 141 141
FT CARBOHYD 146 146
FT CARBOHYD 161 161
FT CARBOHYD 165 165
FT CARBOHYD 191 191
FT CARBOHYD 202 202
FT CARBOHYD 246 246
FT CARBOHYD 267 267
FT CARBOHYD 281 281

FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 343 343 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 626 626 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97140 MW; D197D80940BE732 CRC64;

Query Match 60.3%; Score 123; DB 1; Length 856;
Best Local Similarity 95.8%; Pred. No. 1.2e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOIINMOWEYKAMYAPPISQIR 24
DB 421 KOIINMOWEYKAMYAPPISQIR 444

RESULT 12

ENV_HV1PV STANDARD: PRT; 856 AA.

AC P03376; 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPROTEIN GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retrovirda; Retroviridae; Lentivirus.
OX NCBI_TaxId=11700;

RP MEDLINE=85111157; Pubmed=2962104;
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
RT AIDS/lymphadenopathy retrovirus."
RL Nature 313:450-456(1985).

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DR EMBL: K02083; AAB59873.1; -
DR EMBL: X01762; CAA25903.1; ALT_SEQ.
DR PIR: A03974; VCLJVL.
DR HIV: K02083; ENVSPV22.

DR InterPro: IPR000328; Env-GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.

KW AIDS; Coat protein; Polypotein; Glycoprotein; Transmembrane;
Signal.

FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT CHAIN 512 856 EXTERIOR MEMBRANE GLYCOPROTEIN.
TRANSMEMBRANE GLYCOPROTEIN.

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FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.
FT CARBOHYD 88 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97339 MW; 5FCDB1DC3C120983 CRC64;
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Query Match 60.3%; Score 123; DB 1; Length 856;
Best Local Similarity 95.8%; Pred. No. 1.2e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 KOIINMGEVGMKAPISGOIR 24
Db 421 KOIINMGEVGMKAPISGOIR 444
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RESULT 13
ENV_HV1BR STANDARD; PRT: 861 AA.
AC P03377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099333; PubMed=2981635;
RA Wain-Hobson S., Sonigo P., Danos O., Cole S., Allizon M.;
RA "Nucleotide sequence of the AIDS virus, LAV.";
RA Cell 40:9-17(1985).
CC
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CC EMBL; K02013; AAB59751.1; -
DR EMBL; A04321; CA00352.1; -
DR PIR; A03975; VCLJLV.
DR HTV; K02013; ENV5BRU.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; polypeptide; glycoprotein; Transmembrane;
KW signal.
FT SIGNAL 1 30
FT CHAIN 31 516
FT DISULFID 517 861
FT DISULFID 54 74
FT DISULFID 119 210
FT DISULFID 126 201
FT DISULFID 131 162
FT DISULFID 223 252
FT DISULFID 233 244
FT DISULFID 301 336
FT DISULFID 383 450
FT DISULFID 390 423
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 146 146
FT CARBOHYD 161 161
FT CARBOHYD 165 165
FT CARBOHYD 191 191
FT CARBOHYD 202 202
FT CARBOHYD 235 235
FT CARBOHYD 239 239
FT CARBOHYD 246 246
FT CARBOHYD 267 267
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FT CARBOHYD 361 361
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FT CARBOHYD 453 453
FT CARBOHYD 468 468
FT CARBOHYD 616 616
FT CARBOHYD 621 621
FT CARBOHYD 630 630
FT CARBOHYD 642 642
FT CARBOHYD 679 679
FT CARBOHYD 755 755
FT CARBOHYD 821 821
SQ SEQUENCE 861 AA; 97487 MW; 04DE2B4D4E4F63A CRC64;
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Query Match 60.3%; Score 123; DB 1; Length 861;
Best Local Similarity 95.8%; Pred. No. 1.2e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 KOIINMGEVGMKAPISGOIR 24
Db 426 KOIINMGEVGMKAPISGOIR 449
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[illegible]

FT	CARBOHYD	460	460	N-LINKED (GLCNAC. . .)	(POTENTIAL).					
FT	CARBOHYD	475	475	N-LINKED (GLCNAC. . .)	(POTENTIAL).					
FT	CARBOHYD	622	622	N-LINKED (GLCNAC. . .)	(POTENTIAL).					
FT	CARBOHYD	627	627	N-LINKED (GLCNAC. . .)	(POTENTIAL).					
FT	CARBOHYD	636	636	N-LINKED (GLCNAC. . .)	(POTENTIAL).					
FT	CARBOHYD	648	648	N-LINKED (GLCNAC. . .)	(POTENTIAL).					
SO	SEQUENCE	867 AA;	98399 MW;	5F2310146B8B8680 CRC64;						
Query Match		60.3%;	Score 123;	DB 1;	Length 867;					
Best Local Similarity		95.8%;	Pred. No. 1,3e-09;							
Matches 23;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;					
OY	1 KOIIMMOEVCGRAMPISGQIR 24									
Db	433 KOIIMMOEVCGRAMPISGQIR 456									
RESULT 15										
ENV_HV12										
ID	ENV_HV12	STANDARD;	PRT;	843 AA.						
AC	P35961;									
DT	01-JUN-1994 (Rel. 29, Created)									
DT	01-JUN-1994 (Rel. 29, Last sequence update)									
DT	15-JUL-1999 (Rel. 38, Last annotation update)									
DE	ENVELOPE POLYPROTEIN GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].									
GN	ENV.									
OS	Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).									
OC	Viruses: Retroid viruses; Retroviridae; Lentivirus.									
OX	NCBI_TaxID=36377;									
RN	SEQUENCE FROM N.A.									
RP	MEDLINE=93021387; PubMed=1404605;									
RA	Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H., Shaw G.M.;									
RT	"Complete nucleotide sequence, genome organization, and biological properties of human immunodeficiency virus type 1 in vivo: evidence for limited defectiveness and complementation.";									
RL	J. Virol. 66:6587-6600(1992).									
CC	-----									
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CC	-----									
DR	EMBL; M93258; -; NOT_ANNOTATED_CDS.									
DR	PIR; H44001; H44001.									
DR	InterPro; IPR000328; Env-GP41.									
DR	InterPro; IPR000777; GP120.									
DR	Pfam; PF00516; GP120:1.									
DR	Pfam; PF00517; GP41:1.									
KW	Antib; Coat.protein; Polyprotein; Glycoprotein; Transmembrane; Signal.									
FT	SIGNAL	1	29							
FT	CHAIN	30	489	EXTERIOR MEMBRANE GLYCOPROTEIN.						
FT	CHAIN	490	843	TRANSMEMBRANE GLYCOPROTEIN.						
FT	TRANSMEM	738	755	POTENTIAL.						
FT	DISULFID	53	73	BY SIMILARITY.						
FT	DISULFID	118	201	BY SIMILARITY.						
FT	DISULFID	125	192	BY SIMILARITY.						
FT	DISULFID	130	155	BY SIMILARITY.						
FT	DISULFID	214	243	BY SIMILARITY.						
FT	DISULFID	224	235	BY SIMILARITY.						
FT	DISULFID	292	326	BY SIMILARITY.						
FT	DISULFID	373	432	BY SIMILARITY.						
FT	DISULFID	380	405	BY SIMILARITY.						
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .)						
FT	CARBOHYD	129	129	N-LINKED (GLCNAC. . .)						
FT	CARBOHYD	135	135	N-LINKED (GLCNAC. . .)						

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FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 381 381 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 598 598 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 803 803 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 843 AA; 95648 MW; C69DFD971C918B71 CRC64;
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Query Match 59.8%; Score 122; DB 1; Length 843;
Best Local Similarity 95.8%; Pred. No. 1.7e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 KQIINMGEVKGKAMYAPPISQIR 24
    |||||
Db 408 KQIINMGEVKGKAMYAPPISQIR 431
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Search completed: January 2, 2002, 09:57:58
Job time: 88 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 2, 2002, 09:56:30 ; Search time 22.85 Seconds
(Without alignments)
249.655 Million cell updates/sec

Title: US-09-508-552-2
204
Perfect score: 1 KOIINMDEVGKAMYAPISQIRRIQSGRAFTYIGK 39
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	129	63.2	203	12	09QE99 human immun
2	129	63.2	203	12	09J4T6 human immun
3	128	62.7	263	12	09WD03 human immun
4	128	62.7	396	12	011498 human immun
5	127	62.3	68	12	097748 human immun
6	127	62.3	84	12	09QFG0 human immun
7	127	62.3	103	12	078883 human immun
8	127	62.3	106	12	078887 human immun
9	127	62.3	158	12	073109 human immun
10	127	62.3	158	12	073110 human immun
11	127	62.3	158	12	073111 human immun
12	127	62.3	158	12	073112 human immun
13	127	62.3	158	12	073113 human immun
14	127	62.3	160	12	073114 human immun
15	127	62.3	160	12	073107 human immun
16	127	62.3	160	12	073108 human immun
17	127	62.3	178	12	070611 human immun
18	127	62.3	183	12	070614 human immun
19	127	62.3	183	12	070609 human immun

20	127	62.3	183	12	070616 human immun
21	127	62.3	183	12	070617 human immun
22	127	62.3	183	12	070621 human immun
23	127	62.3	199	12	09JDM8 human immun
24	127	62.3	199	12	09JDM4 human immun
25	127	62.3	199	12	09JDM0 human immun
26	127	62.3	199	12	09JDM8 human immun
27	127	62.3	199	12	09JDM7 human immun
28	127	62.3	199	12	09JDM4 human immun
29	127	62.3	199	12	09JDM2 human immun
30	127	62.3	199	12	09JDM1 human immun
31	127	62.3	199	12	09JDM6 human immun
32	127	62.3	199	12	09JDM5 human immun
33	127	62.3	199	12	09JDM9 human immun
34	127	62.3	199	12	09JDM1 human immun
35	127	62.3	200	12	09JDM6 human immun
36	127	62.3	200	12	09JDM5 human immun
37	127	62.3	200	12	09JDM3 human immun
38	127	62.3	200	12	09JDM9 human immun
39	127	62.3	202	12	09JDM0 human immun
40	127	62.3	202	12	09JDM5 human immun
41	127	62.3	202	12	09JDM4 human immun
42	127	62.3	202	12	09JDM3 human immun
43	127	62.3	202	12	09JDM0 human immun
44	127	62.3	202	12	09JDM6 human immun
45	127	62.3	202	12	09JDM5 human immun

ALIGNMENTS

RESULT 1					
09QE99	PRELIMINARY:	PRT:	203 AA.		
AC 09QE99:					
DT 01-MAY-2000 (TREMBLrel. 13, Created)					
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)					
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).					
CN ENV.					
OS Human immunodeficiency virus type 1.					
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.					
OX NCBI_TaxID=11676;					
RN [1]					
RP SEQUENCE FROM N.A.					
RA Liu S.-L., Mulvania T., Rodrigo A.G., Kosloff B., He X., Shriner D.,					
RA Schacker T., Shea T., Corey L., Mullins J.L.;					
RT "Emergence and Competitive Selection for Human Immunodeficiency Virus					
RT Type-1 Chimeras in Vivo."					
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.					
DR EMBL: AF185336; AAF06409.1; -					
DR InterPro: IPR000777; GP120.					
DR Pfam: PF00516; GP120; 1.					
KW Envelope protein.					
FT NON_TER					
FT NON_TER					
SO SEQUENCE	203 AA;	22702 MW;	7BC57648B5AAN32A	CRC64;	
Query Match	63.2%;	Score 129;	DB 12;	Length 203;	
Best Local Similarity	96.0%;	Pred. No. 6.2e-10;			
Matches	24;	Conservative	1;	Mismatches	0;
				Indels	0;
				Gaps	0;
OY 1 KOIINMDEVGKAMYAPISQIR 25					
DB 147 KOIINMDEVGKAMYAPISGEIR 171					
RESULT 2					
09J4T6	PRELIMINARY:	PRT:	298 AA.		
AC 09J4T6:					
DT 01-OCT-2000 (TREMBLrel. 15, Created)					

01-OCF-2000 (Tremblrel. 15, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98MX.MC06;
RA Rivera-Morales L.G., Novitsky V.A., Vannberg F., Trujillo J.R.,
RT Tamez-Guerra R., Rodriguez-Padilla C., Essex M.,
RL "HIV-1 subtype B is a predominant AIDS virus in Mexico."
DR Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF200860; AAF27370.1; -
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
FT NON_TER 1
FT NON_TER 298
SQ SEQUENCE 298 AA; 33177 MW; D36E9011072499AA CRC64;

Query Match 63.2%; Score 129; DB 12; Length 298;
Best Local Similarity 83.9%; Pred. No. 9.6e-10;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KOIIMMOEYKAMYAPISGQIRRIQSGP 31
DB 210 KOIIMMOEYKAMYAPISGQIRCSNITG 240

RESULT 3
ID O9WDU3 PRELIMINARY; PRT; 263 AA.
AC O9WDU3;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D-DI-02;
RA MEDLINE=9214314; PubMed=10196271;
RA Bagarrelli P., Mazzoia F., Menzo S., Montironi M., Butini L.,
RT Clementi M.;
RT "Host-specific modulation of the selective constraints driving human
RT immunodeficiency virus type 1 env gene evolution."
RL J. Virol. 73:3764-3777(1999).
DR EMBL: AF105560; AAD27170.1; -
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KM Envelope protein.
FT NON_TER 1
FT NON_TER 263
SQ SEQUENCE 263 AA; 29437 MW; 44AD5C3626BE6895 CRC64;

Query Match 62.7%; Score 128; DB 12; Length 263;
Best Local Similarity 96.0%; Pred. No. 1.1e-09;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIIMMOEYKAMYAPISGQIR 25
DB 163 KOIIMMOEYKAMYAPISGQIR 187

RESULT 4
O11498 PRELIMINARY; PRT; 396 AA.

AC O11498;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC Balotta C., Riva C., Violin M., Colombo C., Galli M., Moroni M.;
RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U95401; AAB52747.1; -
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KM Envelope protein.
FT NON_TER 1
FT NON_TER 396
SQ SEQUENCE 396 AA; 44103 MW; 457EC5D0CA1A9E54 CRC64;

Query Match 62.7%; Score 128; DB 12; Length 396;
Best Local Similarity 68.4%; Pred. No. 1.8e-09;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

OY 1 KOIIMMOEYKAMYAPISGQIRRIQSGPRAVITG 38
DB 293 KOIIMMOEYKAMYAPISGQIRCSNITGLILTRVG 330

RESULT 5
ID O97748 PRELIMINARY; PRT; 68 AA.
AC O97748;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92092169; PubMed=1684385;
RA Pang S., Vinters H.V., Akash T., O'Brien W.A., Chen T.S.;
RT "HIV-1 env sequence variation in brain tissue of patients with AIDS-
RT related neurologic disease."
RL J. Acquir. Immune Defic. Syndr. 4:1082-1092(1991).
DR EMBL: M74988; AAB08908.1; -
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KM Envelope protein.
FT NON_TER 1
FT NON_TER 68
SQ SEQUENCE 68 AA; 7662 MW; F5FBDADE121F7D19 CRC64;

Query Match 62.3%; Score 127; DB 12; Length 68;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIIMMOEYKAMYAPISGQIR 24
DB 37 KOIIMMOEYKAMYAPISGQIR 60

RESULT 6
O90FG0 PRELIMINARY; PRT; 84 AA.
AC O90FG0;
DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LF33;
RA MEDLINE=99412391; PubMed=10482626;
RA Morris A., Marsden M., Halcrow K., Hughes E.S., Brettle R.P.,
RA Bell J.E., Simmonds P.;
RT "Mosaic structure of the human immunodeficiency virus type 1 genome
RT infecting lymphoid cells and the brain: evidence for frequent in vivo
RT recombination events in the evolution of regional populations.";
RL J. Virol. 73:8720-8731(1999).
DR EMBL: AF175038; AAF00384.1; -
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW Envelope protein.
FT NON_TER 1
FT SEQUENCE 84 AA; 9369 MW; 789D75FE6FFDBC11 CRC64;
SQ

Query Match 62.3%; Score 127; DB 12; Length 84;
Best Local Similarity 96.0%; Pred. No. 4.3e-10;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOIINMOEVGKAMYAPPISQIR 25
Db 30 KOIINMOEVGKAMYAPPISQIR 54

RESULT 7
078883 PRELIMINARY; PRT; 103 AA.
AC 078883;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE ENVELOPE POLYPROTEIN (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5990;
RA Ou C.Y., Kalish M.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL: L07160; AAB06860.1; -
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW Polypeptide; Envelope protein.
FT NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 11179 MW; 2FD01547FAE76D51 CRC64;

Query Match 62.3%; Score 127; DB 12; Length 103;
Best Local Similarity 100.0%; Pred. No. 5.4e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOIINMOEVGKAMYAPPISQIR 24
Db 51 KOIINMOEVGKAMYAPPISQIR 74

RESULT 8
078887 PRELIMINARY; PRT; 106 AA.
ID 078887
AC 078887;
DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)

DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE ENVELOPE POLYPROTEIN (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5990;
RA Ou C.Y., Kalish M.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL: L07161; AAB06861.1; -
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW Polypeptide; Envelope protein.
FT NON_TER 1
FT NON_TER 106
SQ SEQUENCE 106 AA; 11522 MW; B3ACDB26DB1390D2 CRC64;

Query Match 62.3%; Score 127; DB 12; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOIINMOEVGKAMYAPPISQIR 24
Db 51 KOIINMOEVGKAMYAPPISQIR 74

RESULT 9
073109 PRELIMINARY; PRT; 158 AA.
ID 073109;
AC 073109;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE ENVELOPE GLYCOPROTEIN V3-V5 LOOP REGION (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98160778; PubMed=9499799;
RA Shankarappa R., Gupta P., Learn G.H. Jr., Rodrigo A.G., Ehrlich G.D.,
RA Rinaldo C.R. Jr., Gorry M.C., Millins J.I., Nara P.L.,
RT "Evolution of human immunodeficiency virus type 1 envelope sequences
RT in infected individuals with differing disease progression profiles.";
RL Virology 241:251-259(1998).
DR EMBL: U15842; AAC59210.1; -
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 158
SQ SEQUENCE 158 AA; 17521 MW; 005F9B3BAE1DAE93 CRC64;

Query Match 62.3%; Score 127; DB 12; Length 158;
Best Local Similarity 100.0%; Pred. No. 8.8e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOIINMOEVGKAMYAPPISQIR 24
Db 114 KOIINMOEVGKAMYAPPISQIR 137

RESULT 10
073110 PRELIMINARY; PRT; 158 AA.
ID 073110
AC 073110;
DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)

01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ENVELOPE GLYCOPROTEIN V3-V5 LOOP REGION (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98160778; PubMed=9499799;
RA Shankarappa R., Gupta P., Learn G.H. Jr., Rodrigo A.G.,
Rinaldo C.R. Jr., Gorry M.C., Millins J.I., Nara P.L., Ehrlich G.D.;
RT "Evolution of human immunodeficiency virus type 1 envelope sequences
in infected individuals with differing disease progression profiles.";
RL Virology 241:251-259(1998).
DR EMBL: U15845; AAC59211.1; -;
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW Envelope protein.
FT NON_TER 1
FT 158
SQ SEQUENCE 158 AA; 17551 MW; 0728EB3B4E184B93 CRC64;

Query Match 62.3%; Score 127; DB 12; Length 158;
Best Local Similarity 100.0%; Pred. No. 8.8e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMOWEGKAMYAPPISQIR 24
Db 114 KOIINMOWEGKAMYAPPISQIR 137

RESULT 11
073111 PRELIMINARY: PRT; 158 AA.
AC 073111;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ENVELOPE GLYCOPROTEIN V3-V5 LOOP REGION (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98160778; PubMed=9499799;
RA Shankarappa R., Gupta P., Learn G.H. Jr., Rodrigo A.G.,
Rinaldo C.R. Jr., Gorry M.C., Millins J.I., Nara P.L., Ehrlich G.D.;
RT "Evolution of human immunodeficiency virus type 1 envelope sequences
in infected individuals with differing disease progression profiles.";
RL Virology 241:251-259(1998).
DR EMBL: U15844; AAC59152.1; -;
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW Envelope protein.
FT NON_TER 1
FT 158
SQ SEQUENCE 158 AA; 17551 MW; 0728EB3B4E184B93 CRC64;

Query Match 62.3%; Score 127; DB 12; Length 158;
Best Local Similarity 100.0%; Pred. No. 8.8e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMOWEGKAMYAPPISQIR 24
Db 114 KOIINMOWEGKAMYAPPISQIR 137

RESULT 12
073112 PRELIMINARY: PRT; 158 AA.
AC 073112;
DT 01-AUG-1998 (TREMBlrel. 07, Created)

01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ENVELOPE GLYCOPROTEIN V3-V5 LOOP REGION (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98160778; PubMed=9499799;
RA Shankarappa R., Gupta P., Learn G.H. Jr., Rodrigo A.G.,
Rinaldo C.R. Jr., Gorry M.C., Millins J.I., Nara P.L., Ehrlich G.D.;
RT "Evolution of human immunodeficiency virus type 1 envelope sequences
in infected individuals with differing disease progression profiles.";
RL Virology 241:251-259(1998).
DR EMBL: U15845; AAC59153.1; -;
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW Envelope protein.
FT NON_TER 1
FT 158
SQ SEQUENCE 158 AA; 17551 MW; 0728EB3B4E184B93 CRC64;

Query Match 62.3%; Score 127; DB 12; Length 158;
Best Local Similarity 100.0%; Pred. No. 8.8e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMOWEGKAMYAPPISQIR 24
Db 114 KOIINMOWEGKAMYAPPISQIR 137

RESULT 13
073113 PRELIMINARY: PRT; 158 AA.
AC 073113;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ENVELOPE GLYCOPROTEIN V3-V5 LOOP REGION (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98160778; PubMed=9499799;
RA Shankarappa R., Gupta P., Learn G.H. Jr., Rodrigo A.G.,
Rinaldo C.R. Jr., Gorry M.C., Millins J.I., Nara P.L., Ehrlich G.D.;
RT "Evolution of human immunodeficiency virus type 1 envelope sequences
in infected individuals with differing disease progression profiles.";
RL Virology 241:251-259(1998).
DR EMBL: U15846; AAC59154.1; -;
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW Envelope protein.
FT NON_TER 1
FT 158
SQ SEQUENCE 158 AA; 17551 MW; 0728EB3B4E184B93 CRC64;

Query Match 62.3%; Score 127; DB 12; Length 158;
Best Local Similarity 100.0%; Pred. No. 8.8e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMOWEGKAMYAPPISQIR 24
Db 114 KOIINMOWEGKAMYAPPISQIR 137

RESULT 14
073114 PRELIMINARY: PRT; 158 AA.
AC 073114;

DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN V3-V5 LOOP REGION (FRAGMENT).
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NCBI_TaxId=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98160778; PubMed=9499799;
 RA Shankarappa R., Gupta P., Learn G.H. Jr., Rodrigo A.G.,
 RA Rinaldo C.R., Gorry M.C., Millins J.I., Nara P.L., Ehrlich G.D.;
 RT "Evolution of human immunodeficiency virus type 1 envelope sequences
 RT in infected individuals with differing disease progression profiles.";
 RL Virology 241:251-259(1998).
 DR EMBL: U15847; AAC59155.1; -
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW Envelope protein.
 FT NON_TER 1
 FT NON_TER 158
 SQ SEQUENCE 158 AA; 17551 MW; 0728EB3BAE184B93 CRC64;

Query Match 62.3%; Score 127; DB 12; Length 158;
 Best Local Similarity 100.0%; Pred. No. 8.8e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOIINMDEVGKAMYAPPISQIR 24
 Db 114 KOIINMDEVGKAMYAPPISQIR 137

RESULT 15
 ID 073107 PRELIMINARY; PRT; 160 AA.
 AC 073107.
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN V3-V5 LOOP REGION (FRAGMENT).
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NCBI_TaxId=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98160778; PubMed=9499799;
 RA Shankarappa R., Gupta P., Learn G.H. Jr., Rodrigo A.G.,
 RA Rinaldo C.R., Gorry M.C., Millins J.I., Nara P.L., Ehrlich G.D.;
 RT "Evolution of human immunodeficiency virus type 1 envelope sequences
 RT in infected individuals with differing disease progression profiles.";
 RL Virology 241:251-259(1998).
 DR EMBL: U15840; AAC59208.1; -
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW Envelope protein.
 FT NON_TER 1
 FT NON_TER 160
 SQ SEQUENCE 160 AA; 17688 MW; DE195014562383A9 CRC64;

Query Match 62.3%; Score 127; DB 12; Length 160;
 Best Local Similarity 100.0%; Pred. No. 8.9e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOIINMDEVGKAMYAPPISQIR 24
 Db 116 KOIINMDEVGKAMYAPPISQIR 139

Search completed: January 2, 2002, 09:58:28
 Job Time: 118 sec

Wed Jan 2 10:00:39 2002

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